

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 27, 2006, 17:31:21 ; Search time 188 Seconds
(without alignments)
1269.057 Million cell updates/sec

Title: US-10-676-079-2
Perfect score: 2842
Sequence: 1 MLRSKPALPPLMLLLGP.....LPAFSYFFVIRNAKVAACI 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2842	100.0	543	2	AAy02345 A human h
2	2842	100.0	543	3	Aay57590 Human hep
3	2842	100.0	543	3	Aab08849 Amino aci
4	2842	100.0	543	3	Aay52990 Human hep
5	2842	100.0	543	4	Aay97635 Human hep
6	2842	100.0	543	5	ABb07813 Human hep
7	2842	100.0	543	7	ADG88800 Human hpa
8	2842	100.0	543	8	ADL16379 Human hep
9	2842	100.0	543	8	Adm48716 Human hpa
10	2842	100.0	543	9	Aea42466 Human hep
11	2842	100.0	592	2	AAy02346 A human h
12	2842	100.0	592	3	Aab08850 Amino aci
13	2842	100.0	592	7	ADG88804 Human SK-
14	2842	100.0	592	8	ADL16383 Human hep
15	2842	100.0	592	8	Adm48720 Human SK-
16	2842	100.0	592	9	Aea42461 Human hep
17	2838	99.9	543	2	AAy17082 Human hep
18	2838	99.9	543	4	AAB86206 Human hep
19	2838	99.9	543	7	ADD18950 Human dis
20	2838	99.9	543	8	ADK52086 Human ato
21	2838	99.9	543	8	Adm48759 Human hpa
22	2838	99.9	543	8	ADN05074 Antipsori
23	2838	99.9	543	8	ADN04902 Antipsori
24	2838	99.9	543	8	ADQ80372 Heparanas

25	2838	99.9	543	8	ADR88210	Human pre
26	2838	99.9	543	8	ADP25079	PRO poly
27	2838	99.9	543	8	ADT78177	Human hep
28	2838	99.9	543	9	ADY27036	Human hep
29	2838	99.9	543	9	AEA42426	Human hep
30	2838	99.9	588	2	AAy30124	A human p
31	2832	99.6	543	8	ADO63831	Human hep
32	2832	99.6	543	8	ADO63823	Human hep
33	2832	99.6	543	8	ADO63832	Human hep
34	2832	99.6	543	8	ADO63822	Human hep
35	2826	99.4	543	4	AAB88361	Human mem
36	2826	99.4	543	8	ADO63824	Human hep
37	2826	99.4	543	9	ADY63087	Human clo
38	2821.5	99.3	556	9	ADZ19010	Heparanas
39	2817	99.1	545	6	ABP56822	Human hep
40	2817	99.1	545	7	ADE16012	G-coupled
41	2817	99.1	545	8	ADL93951	Human G-c
42	2804.5	98.7	570	9	ADZ19008	Heparanas
43	2764	97.3	530	2	AAy34173	Human pre
44	2737	96.3	532	2	AAy17083	Seq ID No
45	2692	94.7	527	9	ADZ19004	HepGS4 Co

ALIGNMENTS

RESULT 1
AAy02345
ID AAy02345 standard; protein; 543 AA.
XX AC
XX AAY02345;
DT 09-JUL-1999 (first entry)
XX
DE A human heparanase protein.
XX
KW Heparanase; hp; modulator; heparin-binding growth factor;
KW cellular response; cytokine; cell interaction; plasma lipoprotein;
KW cellular susceptibility; infection; disintegration;
KW neurodegenerative plaque; wound healing; angiogenesis; restenosis;
KW atherosclerosis; inflammation; neurodegenerative disease; neutralise;
KW plasma heparin; micrometastasis; autoimmune lesion; renal failure.
XX
OS Homo sapiens.
XX
XX WO9911798-A3-
XX
PD 11-MAR-1999.
XX
XX 31-AUG-1998; 98WO-US017954.
XX
XX 02-SEP-1997; 97US-00922170.
XX 02-JUL-1998; 98US-00109386.
XX
(INSI-) INSIGHT STRATEGY & MARKETING LTD.
(HADA-) HADASIT MEDICAL RES SERVICES & DEV.
(FRIE/) FRIEDMAN M. M.
XX
XX Pecker I, Vlodavsky I, Feinstein E;
XX
XX WPI; 1999-302255/25.
XX N-PSDB; AAX35648.
XX
XX New human polynucleotide useful for treating angiogenesis, restenosis,
XX and inflammation.
XX
XX Claim 6; Fig 1; 63pp; English.
XX
XX The specification describes a polypeptide having heparanase (hp)
XX activity. The recombinant protein is used as a modulator of heparin-
XX binding growth factors, cellular responses to heparin-binding growth
XX factors and cytokines, cell interaction with plasma lipoproteins,
XX cellular susceptibility to viral, protozoal and bacterial infections or

CC disintegration of neurodegenerative plaques. Heparanase may be useful for
CC conditions such as wound healing, angiogenesis, restenosis,
CC atherosclerosis, inflammation, neurodegenerative diseases, and viral
CC infections. Mammalian heparanase can be used to neutralize plasma
CC heparin, and anti-heparanase antibodies may be applied for
CC immunodetection and diagnosis of micrometastases, autoimmune lesions, and
CC renal failure in biopsy specimens, plasma samples, and body fluids. The
CC present sequence represents human heparanase
XX
XX
SQ Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 2; Length 543;
Best Local Similarity 100.0%; Pred. No. 2.9e-273;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLRSKPALPPPLMLLLGPGPLSPGALPPAQADVVLDLDFDTPQEPHLVSPSFLSVT 60
Db 1 MLLRSKPALPPPLMLLLGPGPLSPGALPPAQADVVLDLDFDTPQEPHLVSPSFLSVT 60
Qy 61 IDANLATDPRFLLILGSPKLTLAGLSPAYLRFGGKTDFLIIDPKKESFEERSYQWS 120
Db 61 IDANLATDPRFLLILGSPKLTLAGLSPAYLRFGGKTDFLIIDPKKESFEERSYQWS 120
Qy 121 QVNQDICKYGIIPDPVEEKLREWPYQQLLREHYQKKFNKSTYSRSSVDVLYTFANC 180
Db 121 QVNQDICKYGIIPDPVEEKLREWPYQQLLREHYQKKFNKSTYSRSSVDVLYTFANC 180
Qy 181 GLDLIFGLNALLRTADLOWNSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Db 181 GLDLIFGLNALLRTADLOWNSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Qy 241 QLGEDYIQLHKLKRSKTFKNAKLYGPDVGQPRRTAKMLKSLKAGGVIDSVTWHYYL 300
Db 241 QLGEDYIQLHKLKRSKTFKNAKLYGPDVGQPRRTAKMLKSLKAGGVIDSVTWHYYL 300
Qy 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA 360
Db 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA 360
Qy 361 AGFWMLDKLGLSARMGIVNRQVFPFGAGNHLVDENFDPLPDVWLSLLFKLVGTVKVL 420
Db 361 AGFWMLDKLGLSARMGIVNRQVFPFGAGNHLVDENFDPLPDVWLSLLFKLVGTVKVL 420
Qy 421 ASVGSKRKLRLVYLHCTNTDNPRYKEGDLTIYAINLHNVTKYLRLPYPSNKQVDKYL 480
Db 421 ASVGSKRKLRLVYLHCTNTDNPRYKEGDLTIYAINLHNVTKYLRLPYPSNKQVDKYL 480
Qy 481 RPLGPHGLLSKSVQLNGLTLKXVDDQTLPPMEKPLRPGSSILGUPAFYSFFVIIRNAKVA 540
Db 481 RPLGPHGLLSKSVQLNGLTLKXVDDQTLPPMEKPLRPGSSILGUPAFYSFFVIIRNAKVA 540
Qy 541 ACI 543
Db 541 ACI 543

RESULT 2
AA57590

ID AA57590 standard; protein; 543 AA.

XX

AC AA57590;

XX

DT 02-MAR-2000 (first entry)

XX

DE Human heparanase.

XX

KW Human; heparanase; hpa; genetic modification; expression; anticancer;
KW angiogenesis; anti-angiogenic; antiproliferative; antiviral; antitumour;
KW anti-atherosclerotic; anti-inflammatory; antineurodegeneration;
KW heparan sulphate; heparin-binding growth factor; tumour angiogenesis;
KW metastasis; wound healing; restenosis; atherosclerosis; inflammation;
KW neurodegeneration; viral infection; cystic fibrosis; cancer; diagnosis;
KW micrometastasis; autoimmune lesion; kidney failure.

XX Homo sapiens.
OS
XX
XX WO9957244-A1.
PN
XX
XX 11-NOV-1999.
PD
XX
XX 29-APR-1999; 99WO-US009256.
PF
XX
XX 01-MAY-1998; 98US-00071618.
PR
XX
XX 02-MAR-1999; 99US-00260038.
PR
XX
XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (FRIE/) FRIEDMAN M M.
PA
XX
XX Ben-Artzi H, Ayal-Hershkovitz M, Yacoby-Zeevi O, Pecker I;
PI Peleg Y, Shlomi Y;
PI
XX
XX WPI; 2000-062144/05.
DR N-PSDB; AAZ39195.
DR
XX
XX Engineered cells that express recombinant heparanase, useful
PT therapeutically, e.g. for treating angiogenesis and to screen for
PT specific inhibitors, potential anticancer agents.
PT
XX
XX Claim 3; Page 107-109; 118pp; English.
PS

CC The present invention describes genetically modified cells (A) containing
CC a polynucleotide (I) that encodes a polypeptide with heparanase activity,
CC and express recombinant heparanase (II). Heparanase cleaves heparan
CC sulphate (HS) at specific intrachain sites, resulting in release of
CC heparin-binding growth factors, enzymes and proteins that are sequestered
CC by HS in basement membranes, extracellular matrix or cell surfaces. It
CC may also be implicated in tumour angiogenesis and metastases. (II) is
CC potentially useful in wound healing and for treating angiogenesis,
CC restenosis, atherosclerosis, inflammation, neurodegeneration, viral
CC infection and cystic fibrosis. It can also be used to neutralise heparin
CC (an alternative to protamine) and to screen for specific inhibitors
CC (potentially useful for treating cancer and metastases). Antibodies
CC raised against (II) are used for immunodetection and diagnosis of
CC micrometastases, autoimmune lesions and kidney failure. (A) provide (II)
CC in large quantities, in a form that is homogeneously processed and
CC activated/neutralised by a dedicated protease. The present sequence
CC represents human heparanase
XX

SQ Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 3; Length 543;
Best Local Similarity 100.0%; Pred. No. 2.9e-273;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLRSKPALPPPLMLLLGPGPLSPGALPPAQADVVLDLDFDTPQEPHLVSPSFLSVT 60
Db 1 MLLRSKPALPPPLMLLLGPGPLSPGALPPAQADVVLDLDFDTPQEPHLVSPSFLSVT 60
Qy 61 IDANLATDPRFLLILGSPKLTLAGLSPAYLRFGGKTDFLIIDPKKESFEERSYQWS 120
Db 61 IDANLATDPRFLLILGSPKLTLAGLSPAYLRFGGKTDFLIIDPKKESFEERSYQWS 120
Qy 121 QVNQDICKYGIIPDPVEEKLREWPYQQLLREHYQKKFNKSTYSRSSVDVLYTFANC 180
Db 121 QVNQDICKYGIIPDPVEEKLREWPYQQLLREHYQKKFNKSTYSRSSVDVLYTFANC 180
Qy 181 GLDLIFGLNALLRTADLOWNSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Db 181 GLDLIFGLNALLRTADLOWNSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Qy 241 QLGEDYIQLHKLKRSKTFKNAKLYGPDVGQPRRTAKMLKSLKAGGVIDSVTWHYYL 300
Db 241 QLGEDYIQLHKLKRSKTFKNAKLYGPDVGQPRRTAKMLKSLKAGGVIDSVTWHYYL 300
Qy 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA 360
Db 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA 360

Db 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTPGKKVWLGETSSAYGGAPLLSDTFA 360
 Qy 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLDPDYWLKLLFKLVGTAKLM 420
 Db 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLDPDYWLKLLFKLVGTAKLM 420
 Qy 421 ASVQGSKRRKRLRVYLHCTNTDNPYKEGDLTYAINALHNVTYKYLRLPYPSNKKQVDKYL 480
 Db 421 ASVQGSKRRKRLRVYLHCTNTDNPYKEGDLTYAINALHNVTYKYLRLPYPSNKKQVDKYL 480
 Qy 481 RPLGPHGLLSKSVQNLGTLKMWDDQTLPLMEKPLRPGSSGLGPAFYSFFVIRNAKVA 540
 Db 481 RPLGPHGLLSKSVQNLGTLKMWDDQTLPLMEKPLRPGSSGLGPAFYSFFVIRNAKVA 540
 Qy 541 ACI 543
 Db 541 ACI 543
 RESULT 3
 AAB08849
 ID AAB08849 standard; protein; 543 AA.
 XX
 AC AAB08849;
 XX
 DT 15-JAN-2001 (first entry)
 XX
 DE Amino acid sequence of a human heparanase polypeptide.
 XX
 KW Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
 KW heparin-binding growth factor; cytokine; neurodegenerative plaque;
 KW wound healing; infection; burn; angiogenesis; restenosis;
 KW atherosclerosis; inflammation; neurodegenerative disease;
 KW Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200052178-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 14-FEB-2000; 2000WO-US003542.
 XX
 PR 01-MAR-1999; 99US-00258892.
 XX
 PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
 PA (FRIE/) FRIEDMAN M M.
 XX
 PI Pecker I, Vlodavsky I, Feinstein E;
 XX
 DR WPI; 2000-579289/54.
 DR N-PSDB; AAAV5051.
 XX
 PT New polynucleotides encoding a polypeptide having heparanase activity,
 PT useful in wound healing and in gene therapy, particularly in treating
 PT tumor, inflammation, autoimmunity, neurodegenerative diseases.
 XX
 PS Claim 22; Fig 1; 152pp; English.
 XX
 CC The present sequence represents a human protein with heparanase catalytic
 CC activity. The heparanase (hpa) polynucleotide is useful in gene therapy,
 CC particularly in treating tumour, inflammation or autoimmunity.
 CC Particularly, the polynucleotide is useful in modulating the
 CC bioavailability of heparin-binding growth factors, cellular responses to
 CC heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
 CC interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular
 CC susceptibility to certain viral and some bacterial and protozoa
 CC infections, or disintegration of neurodegenerative plaques. The
 CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or
 CC radiation burns), and in the treatment of angiogenesis, restenosis,
 CC atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
 CC Straussler Syndrome or Creutzfeldt-Jakob disease), and some viral,

CC bacterial or protozoa infections
 XX
 SQ Sequence 543 AA;
 Query Match 100.0%; Score 2842; DB 3; Length 543;
 Best Local Similarity 100.0%; Pred. No. 2.9e-273;
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLRSRSPALPPPLMLLLGLPLSPGALPRPAQADVLDLDFFTQPLHLVSPSFLSVT 60
 Db 1 MLRSRSPALPPPLMLLLGLPLSPGALPRPAQADVLDLDFFTQPLHLVSPSFLSVT 60
 Qy 61 IDANLATDPRFLILLGSPKRLTLARGLSPAYLRFGGTKTDLIFDPKKESTFEERSYQWS 120
 Db 61 IDANLATDPRFLILLGSPKRLTLARGLSPAYLRFGGTKTDLIFDPKKESTFEERSYQWS 120
 Qy 121 QVNQDICKYGSIPPDVEEKLRLWPYQEQLLLRHYQKKFNSTYSRSSVDVLYTFANCS 180
 Db 121 QVNQDICKYGSIPPDVEEKLRLWPYQEQLLLRHYQKKFNSTYSRSSVDVLYTFANCS 180
 Qy 181 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNENPSFLKKADIFINGS 240
 Db 181 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNENPSFLKKADIFINGS 240
 Qy 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRKTAKMLKSLFKAGGEVIDSVTWHHYL 300
 Db 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRKTAKMLKSLFKAGGEVIDSVTWHHYL 300
 Qy 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTPGKKVWLGETSSAYGGAPLLSDTFA 360
 Db 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTPGKKVWLGETSSAYGGAPLLSDTFA 360
 Qy 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLDPDYWLKLLFKLVGTAKLM 420
 Db 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLDPDYWLKLLFKLVGTAKLM 420
 Qy 421 ASVQGSKRRKRLRVYLHCTNTDNPYKEGDLTYAINALHNVTYKYLRLPYPSNKKQVDKYL 480
 Db 421 ASVQGSKRRKRLRVYLHCTNTDNPYKEGDLTYAINALHNVTYKYLRLPYPSNKKQVDKYL 480
 Qy 481 RPLGPHGLLSKSVQNLGTLKMWDDQTLPLMEKPLRPGSSGLGPAFYSFFVIRNAKVA 540
 Db 481 RPLGPHGLLSKSVQNLGTLKMWDDQTLPLMEKPLRPGSSGLGPAFYSFFVIRNAKVA 540
 Qy 541 ACI 543
 Db 541 ACI 543
 RESULT 4
 AAY52990
 ID AAY52990 standard; protein; 543 AA.
 XX
 AC AAY52990;
 XX
 DT 21-FEB-2000 (first entry)
 XX
 DE Human heparanase protein sequence.
 XX
 KW Human; heparanase; hpa; diagnosis; therapy; tumour; cytostatic;
 KW anti-diabetic; immunomodulatory; anti-inflammatory; nephrotropic;
 KW metastasis; adenocarcinoma; squamous cell carcinoma; teratocarcinoma;
 KW mesothelioma; melanoma; lymphoma; leukemia; cancer; sepsis; diabetes;
 KW inflammation; haemorrhagic nephritis; nephrotic syndrome;
 KW autoimmune disease; anticancer; kidney disease.
 XX
 OS Homo sapiens.
 XX
 PN WO9957153-A1.
 XX
 PD 11-NOV-1999.
 XX
 PF 29-APR-1999; 99WO-US009255.

Db 241 QLGEDYIQLHKLKSTFKNAKLGPDVGPQRRKTAKMLKFLKAGGEVIDSVTHHYYL 300
 Qy 301 NGRATREDFLNPDVLDIFISSVQKVFQVVESTPGKVKWLGESTSSAYGGGAPLLSDTFA 360
 Db 301 NGRATREDFLNPDVLDIFISSVQKVFQVVESTPGKVKWLGESTSSAYGGGAPLLSDTFA 360
 Qy 361 AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENPDPLDYWLSLLFKKLVGTQVLM 420
 Db 361 AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENPDPLDYWLSLLFKKLVGTQVLM 420
 Qy 421 ASVQGSRRKRLRVYLHCTNTDNPRYKEGDLTYAINLHNVTYKRLPYPPFSNKQVDKYL 480
 Db 421 ASVQGSRRKRLRVYLHCTNTDNPRYKEGDLTYAINLHNVTYKRLPYPPFSNKQVDKYL 480
 Qy 481 RPLGPHGLLSKSVQNLGLTLKQVDDQTLPLMEKPLRPGSSGLGPAFSYSEFVIRNAKVA 540
 Db 481 RPLGPHGLLSKSVQNLGLTLKQVDDQTLPLMEKPLRPGSSGLGPAFSYSEFVIRNAKVA 540
 Qy 541 ACI 543
 Db 541 ACI 543

RESULT 6

ABB07813
 ID ABB07813 standard; protein; 543 AA.

AC ABB07813;

DT 03-JUL-2002 (first entry)

XX Human heparanase sequence.

DE Heparanase; catalytic; cytostatic; antiviral; antibacterial; enzyme;
 KW anti-protozoan; neuroprotective; heparin; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..35
 FT Protein /note= "signal peptide"
 FT /note= "mature protein"

XX US2002034810-A1.

XX 21-MAR-2002.

XX 16-AUG-2001; 2001US-00930218.

XX 20-SEP-2000; 2000US-00666390.

XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.

XX Goldshmidt O, Pecker I, Vlodavsky I, Michal I, Zcharia E;

XX WPI; 2002-338926/37.

XX Nucleic acid encoding avian and reptile heparanase polypeptide is useful
 PT to treat various heparin-related disorders and the signal peptide is
 PT useful in production of membrane-targeted or secreted recombinant
 PT proteins.

XX Disclosure; Fig 1a; 39pp; English.

XX The invention relates to an isolated avian and reptile nucleic acid,
 CC encoding a polypeptide with heparanase catalytic activity. The signal
 CC peptide of the nucleic acid can be used to express membrane-associated or
 CC secreted proteins in heterologous expression systems. The encoded
 CC polypeptides can be used to prevent tumour angiogenesis, metastasis and
 CC invasion, and to intervene with pathologies associated with impaired
 CC heparin-binding growth factors, cellular responses to heparin-binding

CC growth factors and cytokines, cell interaction with plasma lipoproteins,
 CC cellular susceptibility to viral, protozoa and bacterial infections or
 CC disintegration of neurodegenerative plaques. The present sequence
 CC represents a human heparanase protein sequence used in similarity studies
 XX
 SQ Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 5; Length 543;
 Best Local Similarity 100.0%; Pred. No. 2.9e-273;
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLRSKAPALPPPLMLLLGLPLSPGALPRPAQADVDLDFDTQEPHLVSPSFLSVT 60
 Db 1 MLRSKAPALPPPLMLLLGLPLSPGALPRPAQADVDLDFDTQEPHLVSPSFLSVT 60
 Qy 61 IDANLATDPRFLILLGSPKLTLAGLSPAYLRGGTKTDPLIFDPKKESTFEERSYQWS 120
 Db 61 IDANLATDPRFLILLGSPKLTLAGLSPAYLRGGTKTDPLIFDPKKESTFEERSYQWS 120
 Qy 121 QVNODICKYGSIPPDVEEKLRLWPYQFOLLREHYOKKFNSTYSRSSVDVLTFFANCS 180
 Db 121 QVNODICKYGSIPPDVEEKLRLWPYQFOLLREHYOKKFNSTYSRSSVDVLTFFANCS 180
 Qy 181 GLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNPNKSLKKADIFINGS 240
 Db 181 GLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNPNKSLKKADIFINGS 240
 Qy 241 QLGEDYIQLHKLKSTFKNAKLYGPDVGPQRRKTAKMLKFLKAGGEVIDSVTHHYYL 300
 Db 241 QLGEDYIQLHKLKSTFKNAKLYGPDVGPQRRKTAKMLKFLKAGGEVIDSVTHHYYL 300
 Qy 301 NGRATREDFLNPDVLDIFISSVQKVFQVVESTPGKVKWLGESTSSAYGGGAPLLSDTFA 360
 Db 301 NGRATREDFLNPDVLDIFISSVQKVFQVVESTPGKVKWLGESTSSAYGGGAPLLSDTFA 360
 Qy 361 AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENPDPLDYWLSLLFKKLVGTQVLM 420
 Db 361 AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENPDPLDYWLSLLFKKLVGTQVLM 420
 Qy 421 ASVQGSRRKRLRVYLHCTNTDNPRYKEGDLTYAINLHNVTYKRLPYPPFSNKQVDKYL 480
 Db 421 ASVQGSRRKRLRVYLHCTNTDNPRYKEGDLTYAINLHNVTYKRLPYPPFSNKQVDKYL 480
 Qy 481 RPLGPHGLLSKSVQNLGLTLKQVDDQTLPLMEKPLRPGSSGLGPAFSYSEFVIRNAKVA 540
 Db 481 RPLGPHGLLSKSVQNLGLTLKQVDDQTLPLMEKPLRPGSSGLGPAFSYSEFVIRNAKVA 540
 Qy 541 ACI 543
 Db 541 ACI 543

RESULT 7

ADG88800
 ID ADG88800 standard; protein; 543 AA.

AC ADG88800;

XX 11-MAR-2004 (first entry)

XX Human hpa protein.

KW Wound healing; heparanase; ulcer; burn; laceration; surgical incision;
 KW necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy.

XX Homo sapiens.

XX US2003161823-A1.

XX 28-AUG-2003.

XX 14-JAN-2003; 2003US-00341582.

XX

PR 31-AUG-1998; 98WO-US017954.
PR 01-MAR-1999; 99US-00258892.
PR 06-FEB-2001; 2001US-00776874.
PR 05-SEP-2001; 2001WO-IL000830.
PR 19-NOV-2001; 2001US-00988113.
XX (ILAN/) ILAN N.
PA (VLOD/) VLODAVSKY I.
PA (YACO/) YACOBY-ZEEVI O.
PA (PECK/) PECKER I.
PA (FEIN/) FEINSTEIN E.
XX
XX
PI Ilan N, Vlodavsky I, Yacoby-Zeevi O, Pecker I, Feinstein E;
XX
XX WPI; 2003-897910/82.
DR N-PSDB; ADG88799, ADG88801, ADG88832.
XX
XX Composition for treating a wound comprising recombinant heparanase is
PT useful to induce or accelerate wound healing and induce or accelerate
PT angiogenesis.
XX
XX Claim 2; SEQ ID NO 10; 143pp; English.
XX
XX The present invention relates to methods and compositions for inducing
CC and/or accelerating wound healing via the catalytic activity of
CC heparanase. The invention is used to induce or accelerate a healing
CC process, particularly of an ulcer, burn, laceration, surgical incision,
CC necrosis, pressure wound, diabetic ulcer and to induce or accelerate
CC angiogenesis. The present sequence is human hpa protein.
XX
XX Sequence 543 AA;
SQ

Query Match 100.0%; Score 2842; DB 7; Length 543;
Best Local Similarity 100.0%; Pred. No. 2.9e-273;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLRSKPALPPLMLLGGPLSPGALPPAQADVVLDFFTOEPLHLVSPFLSVT 60
Db 1 MLLRSKPALPPLMLLGGPLSPGALPPAQADVVLDFFTOEPLHLVSPFLSVT 60
Qy 61 IDANLATDPRFLLILGSPKLTARGLSPAYLRFGTGTDLFIFPKKXTEFEERSYQWS 120
Db 61 IDANLATDPRFLLILGSPKLTARGLSPAYLRFGTGTDLFIFPKKXTEFEERSYQWS 120
Qy 121 QVNQDICKYGSIPDPVEEKLRLWPYQQLLREHYQKFKXNSTYRSRSDVLYTFANCS 180
Db 121 QVNQDICKYGSIPDPVEEKLRLWPYQQLLREHYQKFKXNSTYRSRSDVLYTFANCS 180
Qy 181 GLDLIFGNALLRTADLQWSSNAQLLDYCSSKGYNISWEIGNEPNSFLKKADIFINGS 240
Db 181 GLDLIFGNALLRTADLQWSSNAQLLDYCSSKGYNISWEIGNEPNSFLKKADIFINGS 240
Qy 241 QLGEDIYQLHKLRLKSTFNKAKLYGPDVGQPRRKTAKMLKSPFKAGGVIDSVTWHHYL 300
Db 241 QLGEDIYQLHKLRLKSTFNKAKLYGPDVGQPRRKTAKMLKSPFKAGGVIDSVTWHHYL 300
Qy 301 NGRTRATREDFLNPVDLFISSVQKVFQVWVSTREPCKKWLGETSSAYGGAPLLSDTFA 360
Db 301 NGRTRATREDFLNPVDLFISSVQKVFQVWVSTREPCKKWLGETSSAYGGAPLLSDTFA 360
Qy 361 AGFWMLDKLGLSARMGIEVWVRQVFFGAGNHYLVDENFDPLDYWLKLLFKLVGKTVLM 420
Db 361 AGFWMLDKLGLSARMGIEVWVRQVFFGAGNHYLVDENFDPLDYWLKLLFKLVGKTVLM 420
Qy 421 ASVQGSKRRKLRYLHCTNTDNPRYKEGDLTYALNLHNVTYKLYLRLPYPSNKQVDKYL 480
Db 421 ASVQGSKRRKLRYLHCTNTDNPRYKEGDLTYALNLHNVTYKLYLRLPYPSNKQVDKYL 480
Qy 481 RPLGPHGLLSKSVQLNGTLTKMVDQTLPLMEKPLRPGSSLGLPAFYSFPVIRNAKVA 540
Db 481 RPLGPHGLLSKSVQLNGTLTKMVDQTLPLMEKPLRPGSSLGLPAFYSFPVIRNAKVA 540
Qy 541 ACI 543

Db 541 ACI 543
|||
RESULT 8
ADL16379
ID ADL16379 standard; protein; 543 AA.
XX
XX ADL16379;
AC
XX DT 06-MAY-2004 (first entry)
XX
XX Human heparanase partial protein.
DE
XX Human; heparanase; heparanase-dependent cancer; cancer;
KW autoimmune reaction; inflammation; chromosome 4; enzyme.
XX
XX Homo sapiens.
OS
XX US2003236215-A1.
PN
XX 25-DEC-2003.
PD
XX 09-JUN-2003; 2003US-00456573.
PF
XX 31-AUG-1998; 98WO-US017954.
PR
XX 01-MAR-1999; 99US-00258892.
PR
XX 08-NOV-1999; 99US-00435739.
XX
XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX
XX Pecker I, Vlodavsky I, Feinstein E;
XX WPI; 2004-070610/07.
XX
XX New antisense oligonucleotide hybridizable with a polynucleotide encoding
PT a polypeptide with heparanase activity, useful for treating diseases such
PT as cancer and autoimmune disorders.
XX
XX Claim 3; SEQ ID NO 10; 108pp; English.
XX
XX The invention relates to an antisense oligonucleotide (ASO) comprising a
CC polynucleotide or a polynucleotide analogue of at least 10 bases being
CC hybridisable in vivo, under physiological conditions, with a portion of
CC a polynucleotide strand encoding a polypeptide having heparanase
CC catalytic activity. Also included are a method of in vivo downregulating
CC heparanase activity (comprising administering the ASO in vivo), a method
CC of treating a subject suffering from a pathological condition
CC (characterised by heparanase activity, comprising administering ASO to
CC the subject), a pharmaceutical composition comprising the ASO and a
CC carrier, an antisense nucleic acid construct (comprising a promoter
CC sequence and a polynucleotide sequence directing the synthesis of an
CC antisense RNA sequence of at least 10 bases being hybridisable in vivo,
CC under physiological conditions, with a polynucleotide strand encoding a
CC polypeptide having heparanase catalytic activity), a method of in vivo
CC downregulating heparanase activity (comprising administering in vivo the
CC antisense nucleic acid construct), a pharmaceutical composition
CC comprising the antisense nucleic acid construct and a carrier, and an
CC analogue of at least 10 bases being hybridisable in vivo, under
CC physiological conditions, with a portion of a polynucleotide strand being
CC characterised by forming at least a portion of an untranslated region
CC (UTR) for a polynucleotide strand encoding a polypeptide having
CC heparanase catalytic activity. The methods and compositions of the
CC present invention are useful for the prevention and/or treatment of
CC diseases or conditions associated with aberrant heparanase activity, such
CC as heparanase-dependent cancer, cancer, autoimmune reaction and
CC inflammation. The gene for human heparanase is located on chromosome 4.
XX The present sequence is a human heparanase protein.
SQ Sequence 543 AA;

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Query Match      100.0%; Score 2842; DB 8; Length 543;
Best Local Similarity 100.0%; Pred. No. 2.9e-273;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLRSKALPPPLMLLLGPGALPRPAQADVDLDFDTQPLHLVSPFLSVT 60
Db 1 MLRSKALPPPLMLLLGPGALPRPAQADVDLDFDTQPLHLVSPFLSVT 60

Qy 61 IDANLATDPRFLILGSPKLTLAGLSPAYLRFGGKTDFLIDPKKESTFEERSYQS 120
Db 61 IDANLATDPRFLILGSPKLTLAGLSPAYLRFGGKTDFLIDPKKESTFEERSYQS 120

Qy 121 QVNQDICKYGSIPDPVEEKLRLWPYQEQLLREHYOKKFNSTYSRSSVDVLYTFANCS 180
Db 121 QVNQDICKYGSIPDPVEEKLRLWPYQEQLLREHYOKKFNSTYSRSSVDVLYTFANCS 180

Qy 181 GLDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Db 181 GLDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240

Qy 241 QLGEDYIQLHKLKRSFTFKNAKLYGPDVGQPRRTAKMLKSFLKAGGEVIDSVTWHHYL 300
Db 241 QLGEDYIQLHKLKRSFTFKNAKLYGPDVGQPRRTAKMLKSFLKAGGEVIDSVTWHHYL 300

Qy 301 NGRTATREDFLNPVDLIDFISVQKVFQVVESTPGKKVILGETSSAYGGAPLLSDTFA 360
Db 301 NGRTATREDFLNPVDLIDFISVQKVFQVVESTPGKKVILGETSSAYGGAPLLSDTFA 360

Qy 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLISLLFKLVGTVKLM 420
Db 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLISLLFKLVGTVKLM 420

Qy 421 ASVQGSKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRLPYPSNKKQVDKYL 480
Db 421 ASVQGSKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRLPYPSNKKQVDKYL 480

Qy 481 RPLGPHGLLSKSVQLNGLTLKWVDDQTLPLPMEKPLRPGSSLGLPAPFSYFFVIRNAKVA 540
Db 481 RPLGPHGLLSKSVQLNGLTLKWVDDQTLPLPMEKPLRPGSSLGLPAPFSYFFVIRNAKVA 540

541 ACI 543
541 ACI 543

RESULT 9
ADM48716
ID ADM48716 standard; protein; 543 AA.
AC ADM48716;
XX
XX 03-JUN-2004 (first entry)
XX
XX Human hpa protein #1.
XX
XX Transgenic animal; heparanase; cancer; viral infection; restenosis;
XX neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa;
XX human.
XX
XX Homo sapiens.
XX
XX US2003217375-A1.
XX
XX 20-NOV-2003.
XX
XX 24-FEB-2003; 2003US-00371218.
XX
XX 31-AUG-1998; 98WO-US017954.
XX 01-MAR-1999; 99US-00258892.
XX 06-FEB-2001; 2001US-00776874.
XX 19-NOV-2001; 2001US-00988113.
XX
XX (ZCHA/) ZCHARIA E.
PA

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(VLOD/) VLODAVSKY I.
(METZ/) METZGER S.
(PECK/) PECKER I.
(ILAN/) ILAN N.
(CHAJ/) CHAJEK-SHAUL T.
(GOLD/) GOLDSHMIDT O.

Zcharia E, Vlodavsky I, Metzger S, Pecker I, Ilan N;
Chajek-Shaul T, Goldshmidt O;
WPI: 2004-021918/02.
N-PSDB; ADM48715, ADM48717.

New transgenic non-human animal expressing heparinase, useful as models for human disease, such as cancers, viral infection, neurodegenerative diseases, restenosis, atherosclerosis and pulmonary disorders.

Example 1; SEQ ID NO 10; 106pp; English.

The present invention relates to a transgenic non-human animal whose genome comprises an exogenous polynucleotide sequence, including a promoter active in tissues of the non-human, a region encoding a human heparanase, where the promoter and the region encoding human heparanase are operably linked in the exogenous polynucleotide such that human heparanase is expressed in at least a portion of the cells of the non-human animal. The methods and compositions of the present invention are useful for the production of transgenic animals expressing heparanase, to be used as models for human diseases such as cancers, viral infection, restenosis, neurodegenerative diseases, atherosclerosis and pulmonary disorders. The present sequence is human hpa protein used in the exemplification of the invention.

Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 8; Length 543;
Best Local Similarity 100.0%; Pred. No. 2.9e-273;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLRSKALPPPLMLLLGPGALPRPAQADVDLDFDTQPLHLVSPFLSVT 60
Db 1 MLRSKALPPPLMLLLGPGALPRPAQADVDLDFDTQPLHLVSPFLSVT 60

Qy 61 IDANLATDPRFLILGSPKLTLAGLSPAYLRFGGKTDFLIDPKKESTFEERSYQS 120
Db 61 IDANLATDPRFLILGSPKLTLAGLSPAYLRFGGKTDFLIDPKKESTFEERSYQS 120

Qy 121 QVNQDICKYGSIPDPVEEKLRLWPYQEQLLREHYOKKFNSTYSRSSVDVLYTFANCS 180
Db 121 QVNQDICKYGSIPDPVEEKLRLWPYQEQLLREHYOKKFNSTYSRSSVDVLYTFANCS 180

Qy 181 GLDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Db 181 GLDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240

Qy 241 QLGEDYIQLHKLKRSFTFKNAKLYGPDVGQPRRTAKMLKSFLKAGGEVIDSVTWHHYL 300
Db 241 QLGEDYIQLHKLKRSFTFKNAKLYGPDVGQPRRTAKMLKSFLKAGGEVIDSVTWHHYL 300

Qy 301 NGRTATREDFLNPVDLIDFISVQKVFQVVESTPGKKVILGETSSAYGGAPLLSDTFA 360
Db 301 NGRTATREDFLNPVDLIDFISVQKVFQVVESTPGKKVILGETSSAYGGAPLLSDTFA 360

Qy 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLISLLFKLVGTVKLM 420
Db 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLISLLFKLVGTVKLM 420

Qy 421 ASVQGSKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRLPYPSNKKQVDKYL 480
Db 421 ASVQGSKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRLPYPSNKKQVDKYL 480

Qy 481 RPLGPHGLLSKSVQLNGLTLKWVDDQTLPLPMEKPLRPGSSLGLPAPFSYFFVIRNAKVA 540
Db 481 RPLGPHGLLSKSVQLNGLTLKWVDDQTLPLPMEKPLRPGSSLGLPAPFSYFFVIRNAKVA 540

541 ACI 543
541 ACI 543

QY 541 ACI 543
 DB 541 ACI 543

RESULT 10
 AEA42466
 ID AEA42466 standard; protein; 543 AA.
 XX AC AEA42466;
 XX 28-JUL-2005 (first entry)
 XX Human heparanase protein.
 XX antibody; heparanase; antiinflammatory; vulnery; immunosuppressive;
 KW antiangiogenic; cytostatic; antiarteriosclerotic; vasotropic;
 KW inflammation; wound healing; scarring; vasculopathy; autoimmune disease;
 KW angiogenesis disorder; cancer; tumor; metastasis.
 XX Homo sapiens.
 OS AU2004201462-A1.
 PN 06-MAY-2004.
 PD 08-APR-2004; 2004AU-00201462.
 PF 08-APR-2004; 2004AU-00201462.
 PR (INSI-) INSIGHT BIOPHARMACEUTICALS LTD.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
 XX Vlodavsky I, Pecker I, Miron M, Gilboa A, Miron D, Moskowitz H;
 PI Shlomi Y, Peleg Y, Yacoby-Zeevi O, Ayal-Hershkovitz M, Ben-Artzi H;
 PI Feinstein E;
 XX WPI; 2005-173343/19.
 DR N-PSDB; AEA42465, AEA42434, AEA42435.
 XX Novel isolated antibody capable of specifically binding to epitope of
 PT heparanase protein, useful for preventing and treating heparanase-related
 PT disorder such as inflammatory disorder, scars, autoimmune conditions or
 PT angiogenesis.
 XX Example 8; Fig 47; 260pp; English.

The invention relates to an isolated antibody or its portion (I) capable
 of specifically binding to an epitope of a heparanase protein. Also
 described: (1) a cell line (II) for producing a monoclonal antibody or
 its portion, comprising a cell line for producing (I); (2) a
 pharmaceutical composition comprising (I) and a carrier; and (3) an
 affinity medium (III) for binding human heparanase polypeptides,
 comprising (I) immobilized to a chemically inert, insoluble carrier. (I)
 useful for treating a subject suffering from a pathological condition,
 which involves administering (I) to the subject. (I) is useful for
 preventing and treating heparanase-related disorder or condition chosen
 from inflammatory disorder, wound, scar, vasculopathy, autoimmune
 condition, angiogenesis, cell proliferation, cancerous condition, tumor
 cell proliferation, invasion of circulating tumor cells and metastatic
 disease. (I) is useful for detecting the presence of heparanase
 polypeptide in a sample. (I) is useful for detecting heparanase-related
 disease or condition in a subject such as vertebrate, preferably mammal
 e.g., human. The heparanase-related disorder or condition further
 includes renal disease or disorder chosen from diabetic nephropathy,
 glomerulosclerosis, nephrotic syndrome, minimal change nephrotic syndrome
 and renal cell carcinoma. The present sequence represents human
 heparanase, which is used in the exemplification of the present
 invention.

Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 9; Length 543;
 Best Local Similarity 100.0%; Pred. No. 2.9e-273;
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLRSKDALPPPLMLLLGPGPLSPGALPRPAQAQDVVDLDFPTQBPPLHLVSPSFLSVT 60
 DB 1 MLLRSKDALPPPLMLLLGPGPLSPGALPRPAQAQDVVDLDFPTQBPPLHLVSPSFLSVT 60

QY 61 IDANLATDPRPLILLGSPKLTARGLSPAYLRGGTKTDFLIDPKKESFEERSYQWS 120
 DB 61 IDANLATDPRPLILLGSPKLTARGLSPAYLRGGTKTDFLIDPKKESFEERSYQWS 120

QY 121 QVNODICKYGSIPPDVEEKLRLWPYQQLLLRHHYQKFKNSTYSSRSSVDVLYTFANC 180
 DB 121 QVNODICKYGSIPPDVEEKLRLWPYQQLLLRHHYQKFKNSTYSSRSSVDVLYTFANC 180

QY 181 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNPNPSFLKKADIFINGS 240
 DB 181 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNPNPSFLKKADIFINGS 240

QY 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTWHHYL 300
 DB 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTWHHYL 300

QY 301 NGRTATREDFLNPDVLDIFISSVOKVQVVESTFRPGKVMWLGTSAYGGGAPLLSDTFA 360
 DB 301 NGRTATREDFLNPDVLDIFISSVOKVQVVESTFRPGKVMWLGTSAYGGGAPLLSDTFA 360

QY 361 AGFMWLDKLGSLARMGIEVVMRQVFFGAGNHYLVDENFDPLPDYWLISLLFKKLVGTQVLM 420
 DB 361 AGFMWLDKLGSLARMGIEVVMRQVFFGAGNHYLVDENFDPLPDYWLISLLFKKLVGTQVLM 420

QY 421 ASVQGSRRKRLRVYLHCTNTDNPRYKSGDLTLIYAINLHNVTXYLRLPYPSNKQVDKYL 480
 DB 421 ASVQGSRRKRLRVYLHCTNTDNPRYKSGDLTLIYAINLHNVTXYLRLPYPSNKQVDKYL 480

QY 481 RPLGPHGLLSKSVQNLGLTLKMWDDQTLPLMEKPLRPGSSILGLPAFSYSFFVIENAKVA 540
 DB 481 RPLGPHGLLSKSVQNLGLTLKMWDDQTLPLMEKPLRPGSSILGLPAFSYSFFVIENAKVA 540

QY 541 ACI 543
 DB 541 ACI 543

RESULT 11
 AAY02346
 ID AAY02346 standard; protein; 592 AA.
 AC AAY02346;
 XX 09-JUL-1999 (first entry)
 XX A human heparanase protein.
 KW Heparanase; hpa; modulator; heparin-binding growth factor;
 KW cellular response; cytokine; cell interaction; plasma lipoprotein;
 KW cellular susceptibility; infection; disintegration;
 KW neurodegenerative plaque; wound healing; angiogenesis; restenosis;
 KW atherosclerosis; inflammation; neurodegenerative disease; neutralise;
 KW plasma heparin; micrometastasis; autoimmune lesion; renal failure.
 XX Homo sapiens.
 OS WO9911798-A1.
 XX 11-MAR-1999.
 XX 31-AUG-1998; 98WO-US017954.
 XX 02-SEP-1997; 97US-00922170.
 XX 02-JUL-1998; 98US-00109386.

PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
 PA (FRIE/) FRIEDMAN M M.
 PI Pecker I, Vlodavsky I, Feinstein E;
 XX WPI; 1999-302255/25.
 DR N-PSDB; AAX35650.
 XX
 PT New human polynucleotide useful for treating angiogenesis, restenosis,
 PT and inflammation.
 XX
 PS Claim 6; Page 65-66; 63pp; English.
 CC The specification describes a polypeptide having heparanase (hpa)
 CC activity. The recombinant protein is used as a modulator of heparin-
 CC binding growth factors, cellular responses to heparin-binding growth
 CC factors and cytokines, cell interaction with plasma lipoproteins,
 CC cellular susceptibility to viral, protozoal and bacterial infections or
 CC disintegration of neurodegenerative plaques. Heparanase may be useful for
 CC conditions such as wound healing, angiogenesis, restenosis,
 CC atherosclerosis, inflammation, neurodegenerative diseases, and viral
 CC infections. Mammalian heparanase can be used to neutralize plasma
 CC heparin, and anti-heparanase antibodies may be applied for
 CC immunodetection and diagnosis of micrometastases, autoimmune lesions, and
 CC renal failure in biopsy specimens, plasma samples, and body fluids. The
 CC present sequence represents human heparanase
 XX
 SQ Sequence 592 AA;
 Query Match 100.0%; Score 2842; DB 2; Length 592;
 Best Local Similarity 100.0%; Pred. No. 3.3e-273;
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLRSKALPPPLMLLLGPGPLSPGALPRPAQADVVDLDFFTQPLHLVSPFLSVT 60
 Db 50 MLRSKALPPPLMLLLGPGPLSPGALPRPAQADVVDLDFFTQPLHLVSPFLSVT 109
 Qy 61 IDANLATDPRFLILGSPKLTLAGLSPAYLRFGGKTDFLI FDPKKESTFEERSYQWS 120
 Db 110 IDANLATDPRFLILGSPKLTLAGLSPAYLRFGGKTDFLI FDPKKESTFEERSYQWS 169
 Qy 121 QVNODICKYGSIPPDVEEKLRLWPYQEQLLRLREHYQKFNSTYSRSSVDVLYTFANC 180
 Db 170 QVNODICKYGSIPPDVEEKLRLWPYQEQLLRLREHYQKFNSTYSRSSVDVLYTFANC 229
 Qy 181 GLDLIFGLNALLRTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
 Db 230 GLDLIFGLNALLRTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 289
 Qy 241 QLGEDYIQLHKLKRSFTKNAKLYGPDVGOPRRKTAKWLKSFLLKAGGEVDSVTVHHYLL 300
 Db 290 QLGEDYIQLHKLKRSFTKNAKLYGPDVGOPRRKTAKWLKSFLLKAGGEVDSVTVHHYLL 349
 Qy 301 NGRTATREDFLNPVDLDFI TSSVQKVFQVVESTRPGKKWLGETSAYGGAPLLSDTFA 360
 Db 350 NGRTATREDFLNPVDLDFI TSSVQKVFQVVESTRPGKKWLGETSAYGGAPLLSDTFA 409
 Qy 361 AGFMWLDKLGLSARMGLVEVMRQVFFGAGNYHLVDENFDPLDYWLSLLFKKLVTGKVL 420
 Db 410 AGFMWLDKLGLSARMGLVEVMRQVFFGAGNYHLVDENFDPLDYWLSLLFKKLVTGKVL 469
 Qy 421 ASVGSKRRKLRVYLHCTNTDNPYKEGDLTYA INLHNVTYKLRLPYPSNKKQVDKYL 480
 Db 470 ASVGSKRRKLRVYLHCTNTDNPYKEGDLTYA INLHNVTYKLRLPYPSNKKQVDKYL 529
 Qy 481 RPLGPHGLLSKSVQNLGTLTKWDDQTL PPLMEKPLRPGSSGLPAFYSFFVIRNAKVA 540
 Db 530 RPLGPHGLLSKSVQNLGTLTKWDDQTL PPLMEKPLRPGSSGLPAFYSFFVIRNAKVA 589
 Qy 541 ACI 543
 Db 590 ACI 592

RESULT 12

AAB08850
 ID AAB08850 standard; protein; 592 AA.
 XX
 AC AAB08850;
 XX
 DT 15-JAN-2001 (first entry)
 XX
 DE Amino acid sequence of a human heparanase polypeptide.
 XX
 KW Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
 KW heparin-binding growth factor; cytokine; neurodegenerative plaque;
 KW wound healing; infection; burn; angiogenesis; restenosis;
 KW atherosclerosis; inflammation; neurodegenerative disease;
 KW Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease.
 XX
 OS Homo sapiens.
 XX
 PN WC200052178-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 14-FEB-2000; 2000WO-US003542.
 XX
 PR 01-MAR-1999; 99US-00258892.
 XX
 PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
 PA (FRIE/) FRIEDMAN M M.
 XX
 PI Pecker I, Vlodavsky I, Feinstein E;
 XX
 DR WPI; 2000-579289/54.
 DR N-PSDB; AAA75053.
 XX
 PT New polynucleotides encoding a polypeptide having heparanase activity,
 PT useful in wound healing and in gene therapy, particularly in treating
 PT tumor, inflammation, autoimmunity, neurodegenerative diseases.
 XX
 PS Claim 22; Page 122-123; 152pp; English.
 XX
 CC The present sequence represents a human protein with heparanase catalytic
 CC activity. The heparanase (hpa) polynucleotide is useful in gene therapy,
 CC particularly in treating tumour, inflammation or autoimmunity.
 CC Particularly, the polynucleotide is useful in modulating the
 CC bioavailability of heparin-binding growth factors, cellular responses to
 CC heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
 CC interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular
 CC susceptibility to certain viral and some bacterial and protozoa
 CC infections, or disintegration of neurodegenerative plaques. The
 CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or
 CC radiation burns), and in the treatment of angiogenesis, restenosis,
 CC atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
 CC Straussler Syndrome or Creutzfeldt-Jakob disease), and some viral,
 CC bacterial or protozoa infections
 XX
 SQ Sequence 592 AA;
 Query Match 100.0%; Score 2842; DB 3; Length 592;
 Best Local Similarity 100.0%; Pred. No. 3.3e-273;
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLRSKALPPPLMLLLGPGPLSPGALPRPAQADVVDLDFFTQPLHLVSPFLSVT 60
 Db 50 MLRSKALPPPLMLLLGPGPLSPGALPRPAQADVVDLDFFTQPLHLVSPFLSVT 109
 Qy 61 IDANLATDPRFLILGSPKLTLAGLSPAYLRFGGKTDFLI FDPKKESTFEERSYQWS 120
 Db 110 IDANLATDPRFLILGSPKLTLAGLSPAYLRFGGKTDFLI FDPKKESTFEERSYQWS 169
 Qy 121 QVNODICKYGSIPPDVEEKLRLWPYQEQLLRLREHYQKFNSTYSRSSVDVLYTFANC 180

Db 170 QVNQDICKYGSIPDPVEKLRLEWPFYQEQLLREHYQKKFNSTYSRSSVDVLYTFANCS 229
Qy 181 GLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Db 230 GLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 289
Qy 241 QLGEDYIQLHKLKRSKSTFNKAKLYGPDVGQPRRTAKMLKSFLLKAGGVIDSVTWHHYL 300
Db 290 QLGEDYIQLHKLKRSKSTFNKAKLYGPDVGQPRRTAKMLKSFLLKAGGVIDSVTWHHYL 349
Qy 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTREPKKVMWLGESSAYGGAPLLSDTFA 360
Db 350 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTREPKKVMWLGESSAYGGAPLLSDTFA 409
Qy 361 AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFLLKVLGTVKYL 420
Db 410 AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFLLKVLGTVKYL 469
Qy 421 ASVOGSKRRKLRVYLHCTNTDNPRYKEDLTLYAINLHNVTKYLRPLPYFNSKQVDKYL 480
Db 470 ASVOGSKRRKLRVYLHCTNTDNPRYKEDLTLYAINLHNVTKYLRPLPYFNSKQVDKYL 529
Qy 481 RPLGPHGLLSKSVQLNGLTLLKQVDDQTLPLMEKPLRPGSSGLGPAFYSYSPFVIRNAKVA 540
Db 530 RPLGPHGLLSKSVQLNGLTLLKQVDDQTLPLMEKPLRPGSSGLGPAFYSYSPFVIRNAKVA 589
Qy 541 ACI 543
Db 590 ACI 592

RESULT 13
ADG88804
ID ADG88804 standard; protein; 592 AA.
XX
AC ADG88804;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human SK-hep1 protein.
XX
KW Wound healing; heparanase; ulcer; burn; laceration; surgical incision;
KW necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy.
XX
OS Homo sapiens.
XX
PN US2003161823-A1.
XX
PD 28-AUG-2003.
XX
PF 14-JAN-2003; 2003US-00341582.
XX
PR 31-AUG-1998; 98WO-US017954.
PR 01-MAR-1999; 99US-00258892.
PR 06-FEB-2001; 2001US-00776874.
PR 05-SEP-2001; 2001WO-IL000830.
PR 19-NOV-2001; 2001US-00988113.
XX
PA (ILAN/) ILAN N.
PA (VLQD/) VLQDAVSKY I.
PA (YACO/) YACOBY-ZEEVI O.
PA (PECK/) PECKER I.
PA (FEIN/) FEINSTEIN E.
XX
PI Ilan N, Vlodaysky I, Yacoby-Zeevi O, Pecker I, Feinstein E;
XX
XX WPI; 2003-897910/82.
DR N-PSDB; ADG88803, ADG88805.
XX
XX Composition for treating a wound comprising recombinant heparanase is
PT useful to induce or accelerate wound healing and induce or accelerate
PT angiogenesis.

XX Claim 2; SEQ ID NO 14; 143pp; English.
PS
XX
CC The present invention relates to methods and compositions for inducing
CC and/or accelerating wound healing via the catalytic activity of
CC heparanase. The invention is used to induce or accelerate a healing
CC process, particularly of an ulcer, burn, laceration, surgical incision,
CC necrosis, pressure wound, diabetic ulcer and to induce or accelerate
CC angiogenesis. The present sequence is human SK-hep1 protein.
XX
SQ Sequence 592 AA;
Query Match 100.0%; Score 2842; DB 7; Length 592;
Best Local Similarity 100.0%; Pred. No. 3.3e-273; Indels 0; Gaps 0;
Matches 543; Conservative 0; Mismatches 0;
Qy 1 MLLRSKSPALPPPLMLLLGLPLSPGALPPPAQAQDVVDLDFFTQEPHLVSPSFLSVT 60
Db 50 MLLRSKSPALPPPLMLLLGLPLSPGALPPPAQAQDVVDLDFFTQEPHLVSPSFLSVT 109
Qy 61 IDANLATDPRPLILLGSPKLTTLARGLSPAYLRTGGTKTDFLIIDPKKESTFEERSYQWS 120
Db 110 IDANLATDPRPLILLGSPKLTTLARGLSPAYLRTGGTKTDFLIIDPKKESTFEERSYQWS 169
Qy 121 QVNQDICKYGSIPDPVEKLRLEWPFYQEQLLREHYQKKFNSTYSRSSVDVLYTFANCS 180
Db 170 QVNQDICKYGSIPDPVEKLRLEWPFYQEQLLREHYQKKFNSTYSRSSVDVLYTFANCS 229
Qy 181 GLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Db 230 GLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 289
Qy 241 QLGEDYIQLHKLKRSKSTFNKAKLYGPDVGQPRRTAKMLKSFLLKAGGVIDSVTWHHYL 300
Db 290 QLGEDYIQLHKLKRSKSTFNKAKLYGPDVGQPRRTAKMLKSFLLKAGGVIDSVTWHHYL 349
Qy 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTREPKKVMWLGESSAYGGAPLLSDTFA 360
Db 350 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTREPKKVMWLGESSAYGGAPLLSDTFA 409
Qy 361 AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFLLKVLGTVKYL 420
Db 410 AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFLLKVLGTVKYL 469
Qy 421 ASVOGSKRRKLRVYLHCTNTDNPRYKEDLTLYAINLHNVTKYLRPLPYFNSKQVDKYL 480
Db 470 ASVOGSKRRKLRVYLHCTNTDNPRYKEDLTLYAINLHNVTKYLRPLPYFNSKQVDKYL 529
Qy 481 RPLGPHGLLSKSVQLNGLTLLKQVDDQTLPLMEKPLRPGSSGLGPAFYSYSPFVIRNAKVA 540
Db 530 RPLGPHGLLSKSVQLNGLTLLKQVDDQTLPLMEKPLRPGSSGLGPAFYSYSPFVIRNAKVA 589
Qy 541 ACI 543
Db 590 ACI 592
RESULT 14
ADL16383
ID ADL16383 standard; protein; 592 AA.
XX
AC ADL16383;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heparanase full length protein.
XX
KW Human; heparanase; heparanase-dependent cancer; cancer;
KW autoimmune reaction; inflammation; chromosome 4; enzyme.
XX
OS Homo sapiens.
XX
PN US2003236215-A1.

XX PD 25-DEC-2003.
 XX PF 09-JUN-2003; 2003US-00456573.
 XX 31-AUG-1998; 98WO-US017954.
 PR 01-MAR-1999; 99US-00258892.
 PR 08-NOV-1999; 99US-00435739.
 XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
 XX Pecker I, Vlodavsky I, Feinstein E;
 XX WPI; 2004-070610/07.
 XX New antisense oligonucleotide hybridizable with a polynucleotide encoding
 PT a polypeptide with heparanase activity, useful for treating diseases such
 PT as cancer and autoimmune disorders.
 XX Claim 3; SEQ ID NO 14; 108pp; English.

XX The invention relates to an antisense oligonucleotide (ASO) comprising a
 CC polynucleotide or a polynucleotide analogue of at least 10 bases being
 CC hybridisable in vivo, under physiological conditions, with a portion of
 CC a polynucleotide strand encoding a polypeptide having heparanase
 CC catalytic activity. Also included are a method of in vivo downregulating
 CC heparanase activity (comprising administering the ASO in vivo), a method
 CC of treating a subject suffering from a pathological condition
 CC (characterised by heparanase activity, comprising administering ASO to
 CC the subject), a pharmaceutical composition comprising the ASO and a
 CC carrier, an antisense nucleic acid construct (comprising a promoter
 CC sequence and a polynucleotide sequence directing the synthesis of an
 CC antisense RNA sequence of at least 10 bases being hybridisable in vivo,
 CC under physiological conditions, with a polynucleotide strand encoding a
 CC polypeptide having heparanase catalytic activity), a method of in vivo
 CC downregulating heparanase activity (comprising administering in vivo the
 CC antisense nucleic acid construct), a pharmaceutical composition
 CC comprising the antisense nucleic acid construct and a carrier, and an
 CC antisense oligonucleotide comprising a polynucleotide or a polynucleotide
 CC analogue of at least 10 bases being hybridisable in vivo, under
 CC physiological conditions, with a portion of a polynucleotide strand being
 CC characterised by forming at least a portion of an untranslated region
 CC (UTR) for a polynucleotide strand encoding a polypeptide having
 CC heparanase catalytic activity. The methods and compositions of the
 CC present invention are useful for the prevention and/or treatment of
 CC diseases or conditions associated with aberrant heparanase activity, such
 CC as heparanase-dependent cancer, cancer, autoimmune reaction and
 CC inflammation. The gene for human heparanase is located on chromosome 4.
 CC The present sequence is a human heparanase protein.

XX Sequence 592 AA;

Query Match 100.0%; Score 2842; DB 8; Length 592;
 Best Local Similarity 100.0%; Pred. No. 3.3e-273;
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLRSKALPPPLMLLLGLPLSPGALPPAQADVDLDFPTQPLHLVSPFLSVT 60
 Db 50 MLLRSKALPPPLMLLLGLPLSPGALPPAQADVDLDFPTQPLHLVSPFLSVT 109
 Qy 61 IDANLATDPRFLILGLSPKLTLAGLSPAYLRFGGTKTDFLIDPKKSTFEERSYQWS 120
 Db 110 IDANLATDPRFLILGLSPKLTLAGLSPAYLRFGGTKTDFLIDPKKSTFEERSYQWS 169
 Qy 121 QVNODICKYGSIPDPVEEKLRLWEPYQQLLREHYQKFKNSTYSRSSVDVLYTFANC 180
 Db 170 QVNODICKYGSIPDPVEEKLRLWEPYQQLLREHYQKFKNSTYSRSSVDVLYTFANC 229
 Qy 181 GLDILFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNPNFSFKKADIFNGS 240
 Db 230 GLDILFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNPNFSFKKADIFNGS 289

Qy 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRKTAQMLKSFLLKAGGEVIDSVTHHHYL 300
 Db 290 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRKTAQMLKSFLLKAGGEVIDSVTHHHYL 349
 Qy 301 NGRTATREDFLNPDVLDIFISSVQKVPQVVESTRPGKKWLGGETSSAYGGAPLLSDTEA 360
 Db 350 NGRTATREDFLNPDVLDIFISSVQKVPQVVESTRPGKKWLGGETSSAYGGAPLLSDTEA 409
 Qy 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFKKLVTGTVLM 420
 Db 410 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFKKLVTGTVLM 469
 Qy 421 ASVQSGSKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRLPYPSNKKQVDKYL 480
 Db 470 ASVQSGSKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRLPYPSNKKQVDKYL 529
 Qy 481 RPLGPHGLLSKSVQLNGLTLKMWDDOTLPLMEKPLRPGSSGLGPAFYSFFVTRNAKVA 540
 Db 530 RPLGPHGLLSKSVQLNGLTLKMWDDOTLPLMEKPLRPGSSGLGPAFYSFFVTRNAKVA 589
 Qy 541 ACI 543
 Db 590 ACI 592
 XX ADM48720
 ID ADM48720 standard; protein; 592 AA.
 XX ADM48720;
 AC ADM48720;
 DT 03-JUN-2004 (first entry)
 XX Human SK-hep1 hpa protein.
 DE Human SK-hep1 hpa protein.
 XX Transgenic animal; heparanase; cancer; viral infection; restenosis;
 KW neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa;
 KW human.
 KW Homo sapiens.
 OS Homo sapiens.
 XX US2003217375-A1.
 PN 20-NOV-2003.
 XX 24-FEB-2003; 2003US-00371218.
 PF 31-AUG-1998; 98WO-US017954.
 PR 01-MAR-1999; 99US-00258892.
 PR 06-FEB-2001; 2001US-00776874.
 PR 19-NOV-2001; 2001US-00988113.
 XX (ZCHA/) ZCHARIA E.
 PA (VLOD/) VLODAVSKY I.
 PA (METZ/) METZGER S.
 PA (PECK/) PECKER I.
 PA (ILAN/) ILAN N.
 PA (CHAJ/) CHAJEK-SHAUL T.
 PA (GOLD/) GOLDSHMIDT O.
 XX Zcharia E, Vlodavsky I, Metzger S, Pecker I, Ilan N;
 PI Chajek-Shaul T, Goldshmidt O;
 XX WPI; 2004-021918/02.
 DR N-PSDB; ADM48719, ADM48721.
 XX New transgenic non-human animal expressing heparinase, useful as models
 PT for human disease, such as cancers, viral infection, neurodegenerative
 PT diseases, restenosis, atherosclerosis and pulmonary disorders.
 XX Example 6; SEQ ID NO 14; 106pp; English.
 XX The present invention relates to a transgenic non-human animal whose

CC genome comprises an exogenous polynucleotide sequence, including a
CC promoter active in tissues of the non-human, a region encoding a human
CC heparanase, where the promoter and the region encoding human heparanase
CC are operably linked in the exogenous polynucleotide such that human
CC heparanase is expressed in at least a portion of the cells of the non-
CC human animal. The methods and compositions of the present invention are
CC useful for the production of transgenic animals expressing heparanase, to
CC be used as models for human diseases such as cancers, viral infection,
CC restenosis, neurodegenerative diseases, atherosclerosis and pulmonary
CC disorders. The present sequence is human SK-hepl hpa protein used in the
CC exemplification of the invention.

xx Sequence 592 AA;

Query Match	100.0%;	Score 2842;	DB 8;	Length 592;
Best Local Similarity	100.0%;	Pred. No. 3.3e-273;		
Matches 543;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MLLRKSPALPPPLMLLLGLPLSPGALPRPAQAQDVVDLDFFTQEPHLVSPFSLSVT	60	
Db	50	MLLRKSPALPPPLMLLLGLPLSPGALPRPAQAQDVVDLDFFTQEPHLVSPFSLSVT	109	
Qy	61	IDANLATDPRFLIILGSPKRLTLARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSYWQS	120	
Db	110	IDANLATDPRFLIILGSPKRLTLARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSYWQS	169	
Qy	121	QVNODICKYGIIPDPVEKRLLEWPKYQQLLREHYQKKFNSTYSRSSVDVLYTFANCS	180	
Db	170	QVNODICKYGIIPDPVEKRLLEWPKYQQLLREHYQKKFNSTYSRSSVDVLYTFANCS	229	
Qy	181	GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS	240	
Db	230	GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS	289	
Qy	241	QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSFLKAGGEVIDSVTWHYYL	300	
Db	290	QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSFLKAGGEVIDSVTWHYYL	349	
Qy	301	NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRGKKVWLGETSSAYGGGAPLLSDTFA	360	
Db	350	NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRGKKVWLGETSSAYGGGAPLLSDTFA	409	
Qy	361	AGFWMLDKGLSARMGIEVWVRQVFFGAGNHYLVDENFDPLPDYWLSSLFKLVGTVKVL	420	
Db	410	AGFWMLDKGLSARMGIEVWVRQVFFGAGNHYLVDENFDPLPDYWLSSLFKLVGTVKVL	469	
Qy	421	ASVQSKRRKRLRVYLHCTNTDNPRYKEGDLTYAINLHNVTKYLRLPYPFSNKQVDKYLL	480	
Db	470	ASVQSKRRKRLRVYLHCTNTDNPRYKEGDLTYAINLHNVTKYLRLPYPFSNKQVDKYLL	529	
Qy	481	RPLGPHGLLSKSVQLNGLTLMVDDQTLPLMEKPLRPGSSILGLPAFSYSPFVIRNAKVA	540	
Db	530	RPLGPHGLLSKSVQLNGLTLMVDDQTLPLMEKPLRPGSSILGLPAFSYSPFVIRNAKVA	589	
Qy	541	ACI 543		
Db	590	ACI 592		

Search completed: February 27, 2006, 17:34:45
Job time : 191 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: February 27, 2006, 17:31:41 ; Search time 234 Seconds
(without alignments)
1637.187 Million cell updates/sec
Title: US-10-676-079-2
Perfect score: 2842
Sequence: 1 MLRSKPALPPPLMLLLGP.....LPAFSYFFVIRNAKVAACI 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2838	99.9	543	Q9Y251_HUMAN	Q9Y251 homo sapien
2	2831	99.6	543	Q53GE5_HUMAN	Q53GE5 homo sapien
3	2817	99.1	545	Q9UL39_HUMAN	Q9UL39 homo sapien
4	2282	80.3	545	Q9MY70_BOVIN	Q9MY70 bos taurus
5	2150	75.7	535	Q8K3K3_MOUSE	Q8K3K3 mus musculus
6	2140	75.3	535	Q6YGG1_MOUSE	Q6YGG1 mus musculus
7	2135	75.1	536	Q71RP1_RAT	Q71RP1 rattus norv
8	2123	74.7	536	Q9QZF8_RAT	Q9QZF8 rattus norv
9	1645.5	57.9	523	Q90YK5_CHICK	Q90YK5 gallus gall
10	1317	46.3	533	Q4SYF6_TETNG	Q4SYF6 tetraodon n
11	1154.5	40.6	592	Q9HB37_HUMAN	Q9HB37 homo sapien
12	1151.5	40.5	592	Q5VUH6_HUMAN	Q5VUH6 homo sapien
13	1146.5	40.3	592	Q8WMQ2_HUMAN	Q8WMQ2 homo sapien
14	1040.5	36.6	597	Q4TB80_TETNG	Q4TB80 tetraodon n
15	1021.5	35.9	548	Q5VUH4_HUMAN	Q5VUH4 homo sapien
16	1015.5	35.7	548	Q8WQJ1_HUMAN	Q8WQJ1 homo sapien
17	936.5	33.0	534	Q9HB38_HUMAN	Q9HB38 homo sapien
18	933.5	32.8	534	Q5VUH5_HUMAN	Q5VUH5 homo sapien
19	897.5	31.6	480	Q9HB39_HUMAN	Q9HB39 homo sapien
20	739.5	26.0	255	Q4TGC8_TETNG	Q4TGC8 tetraodon n
21	696	24.5	515	Q8T108_BOMBO	Q8T108 bombyx nori
22	416	14.6	521	Q9SDAL_ARATH	Q9SDAL arabidopsis
23	416	14.6	543	Q9FF10_ARATH	Q9FF10 arabidopsis
24	404	14.2	559	Q89F99_BRAJA	Q89F99 bradyrhizob
25	388	13.7	526	Q5SNA6_ORYSA	Q5SNA6 oryza sativ
26	381	13.4	527	Q9LRC8_SCUBA	Q9LRC8 scutellaria
27	379	13.3	541	Q69116_ORYSA	Q69116 oryza sativ
28	364	12.8	537	Q70YJ3_HORVU	Q70YJ3 hordeum vul
29	363	12.8	536	Q9FZP1_ARATH	Q9FZP1 arabidopsis
30	352.5	12.4	516	Q9FLK8_ARATH	Q9FLK8 arabidopsis
31	352.5	12.4	539	Q8L608_ARATH	Q8L608 arabidopsis

32 350.5 12.3 529 2 Q6ZJE2_ORYSA Q6zje2 oryza sativ
33 169.5 6.0 190 2 Q82604_ARATH Q82604 arabidopsis
34 160 5.6 935 2 Q9VE79_DROME Q9ve79 drosophila
35 141 5.0 559 2 Q7SFB0_NEUCR Q7sfb0 neosporea
36 137 4.8 1128 2 Q5TT65_ANOGA Q5tt65 anopheles g
37 136.5 4.8 463 2 Q63T97_BURPS Q63t97 burkholderi
38 130.5 4.6 493 2 Q9HK01_THEAC Q9hk01 thermoplasma
39 125 4.4 765 2 Q4POC9_USTWA Q4poc9 ustilago ma
40 123 4.3 634 2 Q5NJL7_9BACH Q5njl7 uncultured
41 122.5 4.3 408 2 Q9HEZ1_PHACH Q9hez1 phanerochaete
42 122.5 4.3 408 2 Q9HEZ2_PHACH Q9hez2 phanerochaete
43 122.5 4.3 665 2 Q5SIC3_CRYNE Q5sic3 cryptococcus
44 122.5 4.3 665 2 Q5KV79_CRYNE Q5kv79 cryptococcus
45 120 4.2 511 2 Q55MH5_CRYNE Q55mh5 cryptococcus

ALIGNMENTS

RESULT 1
Q9Y251_HUMAN
ID Q9Y251_HUMAN PRELIMINARY; PRT; 543 AA.
AC Q9Y251_HUMAN
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE Heparanase.
GN Name=HPA; Synonyms=HPSE;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=99321249; PubMed=10395326; DOI=10.1038/10525;
RA Hulett M.D., Freeman C., Hamdorf B.J., Baker R.T., Harris M.J.,
RA Parish C.R.;
RT "Cloning of mammalian heparanase, an important enzyme in tumor
invasion and metastasis.";
RL Nat. Med. 5:803-809 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Vlodavsky I., Friedman Y., Elkin M., Kingorn H., Atzmon R.,
RA Ishai-Michaeli R., Bitan M., Pappo O., Peretz T., Michal I.,
RA Spector L., Pecker I.;
RT "Mammalian heparanase: a novel gene involved in tumor progression and
metastasis.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=99335379; PubMed=10405343; DOI=10.1006/bbrc.1999.0962;
RA Kussie P.H., Hulmes J.D., Ludwig D.L., Patel S., Navarro E.C.,
RA Seddon A.P., Giorgio N.A., Bohlen P.;
RT "Cloning and functional expression of a human heparanase gene.";
RL Biochem. Biophys. Res. Commun. 261:183-187 (1999).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99377052; PubMed=10446189; DOI=10.1074/jbc.274.34.24153;
RA Toyoshima M., Nakajima M.;
RT "Human heparanase. Purification, characterization, cloning, and
expression.";
RL J. Biol. Chem. 274:24153-24160 (1999).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

```
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McWen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Flakesley R.W., Touchan J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RA "Cloned heparanase from MCF-7 cells.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF144325; AAD41342.1; -; mRNA.
DR EMBL; AF152376; AAD45669.1; -; mRNA.
DR EMBL; AF155510; AAD45494.1; -; mRNA.
DR EMBL; AF165154; AAD45379.1; -; mRNA.
DR EMBL; AY948074; AAX47106.1; -; mRNA.
DR EMBL; BC051321; AAH51321.1; -; mRNA.
DR Ensembl; ENSG0000173083; Homo sapiens.
DR GO; GO:0004586; F:beta-glucuronidase activity; TAS.
DR GO; GO:0006029; P:proteoglycan metabolism; TAS.
DR InterPro; IPR005199; Glyco_hydro_79_N.
DR Pfam; PF03662; Glyco_hydro_79n; I.
FT CHAIN 158 543
SQ SEQUENCE 543 AA; 61177 MW; A0262EC267334AB2 CRC64;

Query Match 99.9%; Score 2838; DB 2; Length 543;
Best Local Similarity 99.8%; Pred. No. 1.4e-203;
Matches 542; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLRSKPALPPMLLLGLPLSPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLSVT 60
Db 1 MLLRSKPALPPMLLLGLPLSPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLSVT 60

Qy 61 IDANLATDPRFLILGSPKRLTLARGLSPAYLRFGGTKTDFLIDPKKESTFEERSYQWS 120
Db 61 IDANLATDPRFLILGSPKRLTLARGLSPAYLRFGGTKTDFLIDPKKESTFEERSYQWS 120

Qy 121 QVNQDICKYGSIPDPVEKRLLEWPYQQLLREHYQKFKNSTYSRSSVDVLYTFNACS 180
Db 121 QVNQDICKYGSIPDPVEKRLLEWPYQQLLREHYQKFKNSTYSRSSVDVLYTFNACS 180

Qy 181 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Db 181 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240

Qy 241 OLGEDYIQLHKLKRSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTWHYYL 300
Db 241 OLGEDYIQLHKLKRSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTWHYYL 300

Qy 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTRPCKKVLGETSSAYGGGAPLLSDTFA 360
Db 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTRPCKKVLGETSSAYGGGAPLLSDTFA 360

Qy 361 AGFMWLDKLGLSARGMIEVWVRQVFFGAGNHLVDENFDPLDYWLSLFLFKLVGTKVLM 420
Db 361 AGFMWLDKLGLSARGMIEVWVRQVFFGAGNHLVDENFDPLDYWLSLFLFKLVGTKVLM 420

Qy 421 ASVQGSRRKRLRVYLHCTNTDNPRYKEGDLTLVAINLHNVTKYLRLPYFPSNKKQVDKYLL 480
Db 421 ASVQGSRRKRLRVYLHCTNTDNPRYKEGDLTLVAINLHNVTKYLRLPYFPSNKKQVDKYLL 480

Db 421 ASVQGSRRKRLRVYLHCTNTDNPRYKEGDLTLVAINLHNVTKYLRLPYFPSNKKQVDKYLL 480
Qy 481 RPLGPHGLLSKSVQNLGLTLKMYDDQDTLPPLMEKPLRPGSLGLPAFYSFFVIRNAKVA 540
Db 481 RPLGPHGLLSKSVQNLGLTLKMYDDQDTLPPLMEKPLRPGSLGLPAFYSFFVIRNAKVA 540
Qy 541 ACI 543
Db 541 ACI 543

RESULT 2
Q53GE5 HUMAN PRELIMINARY; PRT; 543 AA.
AC Q53GE5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Heparanase variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human small intestine;
RA Maruyama K., Sugano S.;
RT "Oligo-capping: a simple method to replace the cap structure of
RL eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174 (1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human small intestine;
RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano A., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
RL end-enriched cDNA library.";
RL Gene 200:149-156 (1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human small intestine;
RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK222986; BAD96706.1; -; mRNA.
FT NON_TER 1
SQ SEQUENCE 543 AA; 61118 MW; AC392EC267FC4AB2 CRC64;

Query Match 99.6%; Score 2831; DB 2; Length 543;
Best Local Similarity 99.6%; Pred. No. 4.8e-203;
Matches 541; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLRSKPALPPMLLLGLPLSPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLSVT 60
Db 1 MLLRSKPALPPMLLLGLPLSPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLSVT 60

Qy 61 IDANLATDPRFLILGSPKRLTLARGLSPAYLRFGGTKTDFLIDPKKESTFEERSYQWS 120
Db 61 IDANLATDPRFLILGSPKRLTLARGLSPAYLRFGGTKTDFLIDPKKESTFEERSYQWS 120

Qy 121 QVNQDICKYGSIPDPVEKRLLEWPYQQLLREHYQKFKNSTYSRSSVDVLYTFNACS 180
Db 121 QVNQDICKYGSIPDPVEKRLLEWPYQQLLREHYQKFKNSTYSRSSVDVLYTFNACS 180

Qy 181 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Db 181 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240

Qy 241 OLGEDYIQLHKLKRSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTWHYYL 300
Db 241 OLGEDYIQLHKLKRSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTWHYYL 300

Qy 421 ASVQGSRRKRLRVYLHCTNTDNPRYKEGDLTLVAINLHNVTKYLRLPYFPSNKKQVDKYLL 480
Db 421 ASVQGSRRKRLRVYLHCTNTDNPRYKEGDLTLVAINLHNVTKYLRLPYFPSNKKQVDKYLL 480
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Qy 301 NGRTATREDFLNPVDLIDIFISSVQKVFQVVESTPGKKVWLGETSSAYGGGAPLLSDTFA 360
Db 301 NGRTATREDFLNPVDLIDIFISSVQKVFQVVESTPGKKVWLGETSSAYGGGAPLLSDTFA 360
Qy 361 AGFWLMDKLGLSARMGIEVVMRQVFFGAGNHYLVDPDPLPDYWLKLLFKKLVGTVM 420
Db 361 AGFWLMDKLGLSARMGIEVVMRQVFFGAGNHYLVDPDPLPDYWLKLLFKKLVGTVM 420
Qy 421 ASVQSGSKRRKLRVYLHCTNTDNPRYKEGDLTYAINLHNVTYKLRLLPYFSPSNKQVDKYL 480
Db 421 ASVQSGSKRRKLRVYLHCTNTDNPRYKEGDLTYAINLHNVTYKLRLLPYFSPSNKQVDKYL 480
Qy 481 RPLGPHGLLSKSVQNLGLTLKXVDDQTLPLMEKPLRPGSSLGIPAFYSFFVIRNAKVA 540
Db 481 RPLGPHGLLSKSVQNLGLTLKXVDDQTLPLMEKPLRPGSSLGIPAFYSFFVIRNAKVA 540
Qy 541 ACI 543
Db 541 ACI 543

RESULT 3
Q9UL39_HUMAN
ID Q9UL39_HUMAN PRELIMINARY; PRT; 545 AA.
AC Q9UL39;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Heparanase.
GN Name=HPSE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=20229546; PubMed=10764835; DOI=10.1093/glycob/10.5.467;
RA Dempsey L.A., Plummer T.B., Coombes S.L., Platt J.L.;
RT "Heparanase expression in invasive trophoblasts and acute vascular
RT damage.";
RL Glycobiology 10:467-475 (2000).
DR EMBL; AF084467; AAD54516.1; -; mRNA.
DR Ensembl; ENSG00000173083; Homo sapiens.
DR HGNC; HGNC:5164; HPSE.
DR InterPro; IPR005199; Glyco_hydro_79n.
DR Pfam; PF03662; Glyco_hydro_79n; I.
SQ SEQUENCE 545 AA; 61417 MW; 67B80ACD73CSA9A1 CRC64;

Query Match 99.1%; Score 2817; DB 2; Length 545;
Best Local Similarity 99.4%; Pred. No. 5.4e-202;
Matches 542; Conservative 1; Mismatches 0; Indels 2; Gaps 2;
Qy 1 MLRSKPALPPP-LMLLLGLPLGSPCALPRPAQA-QDVVDLDFFTQEPHLHVSFSL 58
Db 1 MLRSKPALPPPLMLLLGLPLGSPCALPRPAQAQDVVDLDFFTQEPHLHVSFSL 60
Qy 59 VTIDANLATDPRFLILGSPKLRFLARGLSPAYLRFGTGTDFLI FDPKKESTFEERSY 118
Db 61 VTIDANLATDPRFLILGSPKLRFLARGLSPAYLRFGTGTDFLI FDPKKESTFEERSY 120
Qy 119 QSONQDICKYGSIPDPVEEKLRLEWYQEQLLREHYQKKFNSTYSRSSVDVLYTFAN 178
Db 121 QSONQDICKYGSIPDPVEEKLRLEWYQEQLLREHYQKKFNSTYSRSSVDVLYTFAN 180
Qy 179 CSGLDLIFGLNALTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFIN 238
Db 181 CSGLDLIFGLNALTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFIN 240
Qy 239 GSQIGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTWHY 298
Db 241 GSQIGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTWHY 300

Qy 299 YLNGRTATREDFLNPVDLIDIFISSVQKVFQVVESTPGKKVWLGETSSAYGGGAPLLSDT 358
Db 301 YLNGRTATREDFLNPVDLIDIFISSVQKVFQVVESTPGKKVWLGETSSAYGGGAPLLSDT 360
Qy 359 FAAGFWLMDKLGLSARMGIEVVMRQVFFGAGNHYLVDPDPLPDYWLKLLFKKLVGTVM 418
Db 361 FAAGFWLMDKLGLSARMGIEVVMRQVFFGAGNHYLVDPDPLPDYWLKLLFKKLVGTVM 420
Qy 419 LMASVQSGSKRRKLRVYLHCTNTDNPRYKEGDLTYAINLHNVTYKLRLLPYFSPSNKQVDK 478
Db 421 LMASVQSGSKRRKLRVYLHCTNTDNPRYKEGDLTYAINLHNVTYKLRLLPYFSPSNKQVDK 480
Qy 479 LRLPGLPHGLLSKSVQNLGLTLKXVDDQTLPLMEKPLRPGSSLGIPAFYSFFVIRNAK 538
Db 481 LRLPGLPHGLLSKSVQNLGLTLKXVDDQTLPLMEKPLRPGSSLGIPAFYSFFVIRNAK 540
Qy 539 VAACI 543
Db 541 VAACI 543

RESULT 4
Q9MY10_BOVIN
ID Q9MY10_BOVIN PRELIMINARY; PRT; 545 AA.
AC Q9MY10;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Heparanase.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=21176669; PubMed=11277877;
RA Kizaki K., Nakano H., Nakano H., Takahashi T., Imai K., Hashizume K.;
RT "Expression of heparanase mRNA in bovine placenta during gestation.";
RL Reproduction 121:573-580 (2001).
DR EMBL; AF281160; AAF87301.2; -; mRNA.
DR InterPro; IPR005199; Glyco_hydro_79n.
DR Pfam; PF03662; Glyco_hydro_79n; I.
SQ SEQUENCE 545 AA; 61076 MW; FAC4BDFD855B933 CRC64;

Query Match 80.3%; Score 2282; DB 2; Length 545;
Best Local Similarity 79.8%; Pred. No. 6.1e-162;
Matches 435; Conservative 35; Mismatches 73; Indels 2; Gaps 1;
Qy 1 MLRSKPALPPP-LMLLLGLPLGSPCALPRPAQAQDVVDLDFFTQEPHLHVSFSL 58
Db 1 MLACRPGURPPPLLLGLPLGSPCALPRPAQAQDVVDLDFFTQEPHLHVSFSL 60
Qy 59 VTIDANLATDPRFLILGSPKLRFLARGLSPAYLRFGTGTDFLI FDPKKESTFEERSY 118
Db 61 FTIDANLATDPRFTFLGSSKLRFLARGLSPAYLRFGGNGKDFLI FDPKKEPAFEERSY 120
Qy 119 QSONQDICKYGSIPDPVEEKLRLEWYQEQLLREHYQKKFNSTYSRSSVDVLYTFAN 178
Db 121 LSQSNQDICKSGSIPSDVEEKLRLEWYQEQVLLREYQKKFTNSTYSRSSVDVLYTFAS 180
Qy 179 CSGLDLIFGLNALTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFIN 238
Db 181 CSGLDLIFGLNALTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFQKAGIFIN 240
Qy 239 GSQIGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTWHY 298
Db 241 GROLGEDYIFRKLKLSKSAFKNAKLYGPDIGQPRRTVLMKSLFKAGGEVIDSVTWHY 300
Qy 299 YLNGRTATREDFLNPVDLIDIFISSVQKVFQVVESTPGKKVWLGETSSAYGGGAPLLSDT 358
Db 301 YLNGRTATREDFLNPVDLIDIFISSVQKVFQVVESTPGKKVWLGETSSAYGGGAPLLSDT 360

Db 301 YVNGRIATKDFLNPDLIDTDFISSVQKTRIVEKIRPLKVKWLGETSSAFGGGAPFLSNT 360
Qy 359 FAAGFMWLDKGLSARMGIEVWNRQVFPAGNYHLVDENFPDPLDYWLISLLFKKLVGTKV 418
Db 361 FAAGFMWLDKGLSARMGIEVWNRQVLFAGNYHLVDGNFPDPLDYWLISLLFKKLVGKVK 420
Qy 419 LMASVQSGSKRRKLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRPLPYFPFSNKQVDKY 478
Db 421 LMASVKGDPDRSKFRVYLHCTNTKHPRYKEGDLTLVAINLHNVTKYLRPLPHLPHKQVDKY 480
Qy 479 LLRLPGLHLLSKSVQLNGLTLKMWDDQTLPLMEKPLRPGSSGLPFPFSYFFVIRNAK 538
Db 481 LKPSGTDLGLSKSVQLNGLKMWDEQTLPALTEKPLHPGSSGLMPFPFSYFFVIRNAK 540
Qy 539 VAACI 543
Db 541 VAACI 545
RESULT 5
Q8K3K3_MOUSE
ID Q8K3K3_MOUSE PRELIMINARY; PRT; 535 AA.
AC Q8K3K3;
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Heparanase (Mus musculus 0 day neonate thymus cDNA, RIKEN full-length
DE enriched library, clone:A43010M04 product:heparanase, full insert
DE sequence).
GN Name:Hpspe; Synonyms:Hpa, Hspe;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FBV;
RA Miao H.-Q., Navarro E., Patel S., Sargent D., Koo H., Wan H.,
RA Plata A.-Q., Zhou Q., Ludwig D., Bohlen P., Russie P.;
RA "Cloning, expression, and purification of mouse heparanase";
RA protein Expr. Purif. 0:0-0(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning";
RA Meth. Enzymol. 303:19-44(1999).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischer M.W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).

RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12468851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grummond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tonita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [8]
RP NUCLEOTIDE SEQUENCE.

RESULT 6
Q6YGL1_MOUSE
ID Q6YGL1_MOUSE PRELIMINARY; PRT; 535 AA.
AC Q6YGL1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hepatanase.
DE Name:Hpsse;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22841152; PubMed=12837765; DOI=10.1074/jbc.M300925200;
RX Gong F., Jenth P., Galvis M.L.E., Vlodavsky I., Horner A., Lindahl U.,

Qy	13	IMLLLLGPLGPLSGALPRPQAQDVVDLFFFTQEPHLHVSFSLSVTIDANLATDRPFL	72
Db	5	LLLWLWGPIGALAAQAGAPGAPTDDVVDLEFYTKRPLRSVSPSLTIDASTADRPFL	64
Qy	73	ILLGSPKLRTLARGLSPAYLRFGGTKTDFLIPDPKKESTPEERSYWGOSQVNDTCKYGS	132
Db	65	TFLGSPRLRALARGLSPAYLRFGGTKTDFLIPDPKKEPTBEERSYWKOSQVNHDTCRSEPV	124
Qy	133	PPDVEEKLRLWPYQEOQLLREHYOKFKFNSTYSRSSVDVLYTFANCSGGLDILFGLNALL	192
Db	125	SAAVLRKLQVWFPOEQLLRLREYQOKFKFNSTYSRSSVDMDLYSFAKCSGLDLIFGLNALL	184
Qy	193	RTADLQWNSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGSQGEDYIQLHKL	252
Db	185	RTPDLRWNSNAQLLLDYCSSRGYNISSSELGNEPNSFMKKAHILLINGSQGEDVFELHKL	244
Qy	253	LRKSTFKNAKLYGPDVQOPRRKTAOKLSFLKAGGEVIDSVTHHHYILNGRTATREDPLN	312
Db	245	LORSAFQNAKLYGPDIGOPRGKTVKLRSLFKAGGEVIDSLTWHYILNGRIATKEDFLS	304
Qy	313	PDVLDTFISSQVKQVQVVESTRCKKVMKGTSAYGGAPLSDTFAAGPMWLDKLGLS	372
Db	305	SDVLDTFILSQVKILVTKTEITPGKKVMKGKTSAYGAGAPLSDNTFAAGPMWLDKLGLS	364
Qy	373	ARMGIEVVMQVFPFAGNYHLVDENFDPLPDYWLSSLFKKLVGPKVLMAASYGSKRKLRL	432
Db	365	AQMGIEVVMQVFPFAGNYHLVDENFEPDYLWLSLLFKKLVGPRVLLSRVKGPRSKLRL	424
Qy	433	VYLHCTNTDNPRYKEGBDTLTYAILNLHNVTLYKLYRPLPYPSNKQVDKYLLRPLGPHGLSKS	492
Db	425	VYLHCTNVYHPRYQEGDGLTYLVNLHNVTLYKLVPPPLFRPKPVDVTLKPKSGPDGLLSKS	484
Qy	493	VQLNGLTLQWVDQOTLPPMLEKPLRPGSSLGLPAFYSYFFVIRNAKVAACI	543
Db	485	VQLNGQTLKQWDBQTLPALTEKPLPAGSALSPLAFSYGFFVIRNAKVAACI	535

RESULT 7			
Q71RP1_RAT	Q71RP1_RAT	PRELIMINARY;	PRT; S36 AA.
AC	Q71RP1;		
DT	05-JUL-2004	(T-EMBLrel. 27,	Created)
DT	05-JUL-2004	(T-EMBLrel. 27,	Last sequence update)
DT	05-JUL-2004	(T-EMBLrel. 27,	Last annotation update)
DE	Heparanase.		
GN	Name:Hpsg; Synonyma:Hape;		
OS	Rattus norvegicus (Rat)		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Murinae; Rattus.		
OC	NCBI_TaxID=10116;		
OC	[1]		
RN	NCLEOTIDE SEQUENCE.		
RP			
RA	Hulett M.D., Wang J., Hornby J.R., Freeman C., Pagler E., McHenry J.,		
RA	Parish C.R.;		

Query Match 57.9%; Score 1645.5; DB 2; Length 523;
 Best Local Similarity 60.2%; Pred. No. 2.5e-114;
 Matches 320; Conservative 87; Mismatches 114; Indels 11; Gaps 3;

13 LMLLLGLPLSLGALPRPAQADVDLDFTOEPLHLVSPSLVTIDANLATDPREL 72
 2 LVLLLVLLAVPP-----RRTAELQLGRLREPGVSPALSLTDLASLARDPRFV 52
 73 ILGSPKRLTLARGLSPAYLRFQGTCTDFLIFDPKKESTPEERSYQSQVNDICKYGSI 132
 53 ALLRHPLKHLTLASGLSPGLRFQGTSTDFLIFNPKDSTWEEKVSEFQA-KOVCEAWPS 111
 133 PPVVEEKLRLWEPYQOEQLLREHLYQKFKNSTYSSRSVDVLYTFANCSGLDLIFGLNALL 192
 112 FAVVPKLLLTQWPLQOEKLLAEHSMKKHNTTITRSTLDLHTFASSSGFLVFLGNALL 171
 193 RTADLWNSSNAOLLLDYCCSKGYNISWELGNEPNSFKKADIFINGSOLGEDYIOLHKL 252
 172 RRAGLWSSNAKQLLGYCAQRSYNIWELGNEPNSFRKSGICIDFQGLORDFVHLRQL 231
 253 L-RKSTFKNAKLYGPDVQPPRRKTAKMLKSPFKAGGEVIDSVTHHYLYLNGRTATREDFL 311
 232 LSQHPLYRHAELYGLDVQPKKTHLLRSPMKSGRAIDSVTHHYLYVNGRSATREDFL 291
 312 NPVDLDFISVQVQVQVSTRGKKVWLGESTSSAYGGGAPLSDTFAAGFMWLDKGL 371
 292 SPEVLDSPATVHIDVGLVEATVPGKVLGCTGSAVGGAPQVLSNTYVAGFMWLDKGL 351
 372 SARWIEVWVQVFGAGNHLVDENFDPLDYWLKLLFKLVGKLVKMASVQSKERKL 431
 352 AARGIDVWVQVFGAGNHLVDENFDPLDYWLKLLFKLVGKLVKMASVQSKERKL 411
 432 RVLHCTNTDNPYKKEGDLTYALNHNVTYKLRPLPFGSKQVQVYLLRPLGPHGLLSK 491
 412 RVLHCTNPHPKYREGDVTLPALNLSVQSLQPKQLSKSVQVYLLRPLGPHGLLSK 471
 492 SVQLNGLTKMVDQTLPLMEKPLRPGSSGLPAPFSYFVIRNAKVAACI 543
 472 EVQLNGRLQWDDVETLPAHLMALAPGTLGLPAPFSYFVIRNAKVAACI 523

RESULT 10
 Q4SYF6_TETNG PRELIMINARY; PRT; 533 AA.
 AC Q4SYF6;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome undetermined SCAF12073, whole genome shotgun sequence.
 DE (Frames)
 GN ORFNames=GSTENG0010356001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallou O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segures B.,
 RA Desailly C., Salanoubat M., Levy M., Boudet N., Caetellano S.,
 RA Anthonard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Blemont C., Skalli Z., Cottolico L., Poullain J., De Berardinis V.,
 RA Crnaud C., Duprat S., Brotti L., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter E., Quetier F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissenbach J., Roest Croliis H.;
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype."

RL Nature 431:946-957 (2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAE01012073; CAF94326.1; -; Genomic_DNA.
 FT NON_TER 1 533
 FT NON_TER 533
 SQ SEQUENCE 533 AA; 60100 MW; 9800A7C8780100FF CRC64;

Query Match 46.3%; Score 1317; DB 2; Length 533;
 Best Local Similarity 50.0%; Pred. No. 1e-89;
 Matches 268; Conservative 83; Mismatches 141; Indels 44; Gaps 8;

49 LHLVSPSLVTIDANLATDPRELILGSPKLTARGLSPAYLRFQGTCTDFLIPPK 108
 1 LRRVDFRFLSVTIDASLAADERFMYLLSSPKVTLAKALTPAFLRFGGTQDFMVFAPHK 60
 109 E---STFEERSYQSQVNDICKYGSIPTDVEEKLRLWEPYQOEQLLREHLYQKFKNSTY 165
 61 NQPASGFSARELTFSSNGQHSCEWAPPPWLERRLRTEWKKQWMLRNEBQLRKYRVK 120
 166 SRSSVDVLYTFANCSGLDLIFGLNALLRTADLQWSSNAOLLLDYCSSKGYNISWELGNE 225
 121 TETTVQHLAFANCSGLDLVFLGNALLRTADLQWSSNAOLLLDYCSSKGYNISWELGNE 180
 226 PNSFLKADIFINGSOLGEDYIOLHKLKSTF-KNAKLYGPDVQVQVSTRGKKVWLG 284
 181 PMSYEKAGLRLDGRQLGEDFTVLRKILRESRYRDAGLFGPDVQVQVSTRGKKVWLG 240
 285 AGGEVIDSVTHHYLYLNGRTATREDFLNPDVLDIFISSVQVQVSTRGKKVWLG 344
 241 SGAEVADACTWHHYLYLNGRTATREDFLNPDVLDIFISSVQVQVSTRGKKVWLG 300
 345 SSAYGGGAPLSDTFAAGFMWLDKGLSARMGIEVWVQVFFGAGNHLVDENFDPLP-- 402
 301 SSAYGGGAGLSDTFVAGFMWLDKGLAATLGLVLRQVLIAGSYHLDDNDLPLPS 360
 403 -----DYWLSLFLKLVGTVKLVMA-----SVQSGKRRKRLRVYLHCTNTD----- 442
 361 GLLLQDYWLSLFLKLVGTVKLVMA-----SVQSGKRRKRLRVYLHCTNTD----- 418
 443 -----PRYKEGDLTYALNHNVTYKLRPLPFGSKQVQVYLLRPLGPHGLLSK 487
 419 QRKEARFSLVSLCSYRSGAATLMSMNLKQAPRISUPRILSSSTVEAFVLESEQP--GEEG 477
 488 LLSKSVQLNGLTKMVDQTLPLMEKPLRPGSSGLPAPFSYFVIRNAKVAACI 543
 478 LRSRAVKLNGRLVLRWVDDVETLPAHLMALAPGTLGLPAPFSYFVIRNAKVAACI 533

RESULT 11
 Q9HB37_HUMAN PRELIMINARY; PRT; 592 AA.
 AC Q9HB37;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hepatanase-like protein HPA2c.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=20483645; PubMed=11027606; DOI=10.1006/bbr.2000.3586;
 RA McKenzie E., Tyson A., Stamps A., Smith P., Turner P., Barry R.,
 RA Hircok M., Patel S., Barry E., Stubbfield C., Terrett J., Page M.;
 RT "Cloning and expression profiling of Hpa2, a novel mammalian

```
RT heparanase family member." ;
RL Biochem. Biophys. Res. Commun. 276:1170-1177 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA McKenzie E.A., Tyson K., Stamps A.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282887; AAG23423.1; -; mRNA.
DR GO; GO:0005622; C:intracellular; TAS.
DR GO; GO:0030305; F:heparanase activity; TAS.
DR InterPro; IPR005199; Glyco_hydro_79n.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 592 AA; 66580 MW; 95C384AD9A74258E CRC64;

Query Match 40.6%; Score 1154.5; DB 2; Length 592;
Best Local Similarity 43.6%; Pred. No. 1.7e-77;
Matches 250; Conservative 82; Mismatches 189; Indels 53; Gaps 9;

QY 20 PLGLPLSPGAL-----PRPA-----QAQDVVDLDFFTOEPLHLVSPS 55
Db 18 PPACIAPGALYIALLLHLSLSQAGDRPLPVDRAAGLKEKTLILLDVSTKNPVRTVNE 77

QY 56 FLSVTIDANLATDPRFLILLGSPKRLTLARGLSPAYLRFGGTKTDFLIF-----DPKKEST 111
Db 78 FLSLQLDPSIIHD-GWLDLFLSSKELVTLARGLSPAFRLFQGGKRTDFLQFQNLNPAKSRG 136

QY 112 FEERSYQSQVNQDI-----CKYGSIPDPVEEKLRLWPYQEQQL-LLREHYQK 158
Db 137 GPGPDYLLKNYEDDIVRSQVALDRQKQCKIAQ-HPDVMLELQREKAAQMHVLVLLKEQFSN 195

QY 159 KFKNSTYSRSSVDVLYTFANCSGDLIFGLNALLRTADLOWNSSNAQLLLDYCSSKGNYI 218
Db 196 TYSNLIITARSLLKLYNFADCSGLHLIFALNALRRPNNSWSSALSLLKYASKKNI 255

QY 219 SWELGNPNPSFLKKADIFINGSQLGEDIYIQLHKLRLK-STFKNAKLYGPDYQPPRKTK 277
Db 256 SWELGNPNNYRTMHWGRAVNGSQLGKDYIQLKSLQPIRIYSRASLYGNIGRPKKNVIA 315

QY 278 MLKSLKAGGEVIDSVTHVHYLYNGRTATREDFLNPVDLDFISSQVKQFQVWVSTRGK 337
Db 316 LLGDFMKVAGSTVDATVTHQCYIDGRVVKVWDFLKLRLDLSLQDQIRKIQKVNTYTPGK 375

QY 338 KVMIGETSSAYGGGAPLSDTPAAGFMWDLKGLSARMGIEVWRQVFFGAGNTHLVDPEN 397
Db 376 KIWLEGVYTSAGGTNNLSDSYAAGFLWNLTLGLMANGIDVIRHSFFDHGYNHLVDQN 435

QY 398 FDPDPYWLSSLFKKLVGTQKVLMAVSQGSRR-----KLRYVLIHCTNTNDNRYKEG 448
Db 436 FNPLPDYWLSSLYKRLIGPKVLAVHVGQLRQKPRGPRVIRDKLRIYAHCTNHHNHNHYVRG 495

QY 449 DLTLYAINLHNVTYKLYRLPYFSPKQVDKYLRLPLGPHGLLSKSVOLNGLTLKWVDDOTL 508
Db 496 SITFIILNHRSRKKIKLAGTLRDKLVHGYLLQPYGQGLSKSVQLNGQPLVMVDDGTL 555

QY 509 PPLMEKPLRPGSSGLPAPFSYFFVIRNAKVAAC 542
Db 556 PELKPRPLRAGRTLVPVPTWGGFFVVKVNNALAC 589
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RESULT 12
Q5VUH6 HUMAN PRELIMINARY; PRT; 592 AA.
AC Q5VUH6;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Heparanase 2.
GN Name=HPS2; ORFNames=RP11-439D8.2-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP NUCLEOTIDE SEQUENCE.
RA Doggett S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Holt K.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Heath P.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Smith M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL590036; CAH73137.1; -; Genomic DNA.
DR EMBL; AL439243; CAH73137.1; -; Genomic DNA.
DR EMBL; AL4356268; CAH70448.1; -; Genomic DNA.
DR EMBL; AL445251; CAH70448.1; -; Genomic DNA.
DR EMBL; AL4356220; CAH7160.1; -; Genomic DNA.
DR EMBL; AL439243; CAH73137.1; JOINED; Genomic DNA.
DR EMBL; AL4356220; CAH73137.1; JOINED; Genomic DNA.
DR EMBL; AL4356268; CAH73137.1; JOINED; Genomic DNA.
DR EMBL; AL4356268; CAH70448.1; JOINED; Genomic DNA.
DR EMBL; AL445251; CAH7160.1; JOINED; Genomic DNA.
DR EMBL; AL439243; CAH7160.1; JOINED; Genomic DNA.
DR EMBL; AL4356220; CAH7160.1; JOINED; Genomic DNA.
DR EMBL; AL4356220; CAH70448.1; JOINED; Genomic DNA.
DR EMBL; AL439243; CAH70448.1; JOINED; Genomic DNA.
DR EMBL; AL4356268; CAH70448.1; JOINED; Genomic DNA.
DR EMBL; AL4356220; CAH70448.1; JOINED; Genomic DNA.
DR EMBL; AL4356220; CAH7160.1; JOINED; Genomic DNA.
DR EMBL; AL445251; CAH73137.1; JOINED; Genomic DNA.
DR EMBL; AL445251; CAH73137.1; JOINED; Genomic DNA.
DR EMBL; ENSG00000172987; Homo sapiens.
DR HGNC; HGNC:18374; HPS2.
DR InterPro; IPR005199; Glyco_hydro_79n.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 592 AA; 66596 MW; 95C384AD9A6C868E CRC64;
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Query Match 40.5%; Score 1151.5; DB 2; Length 592;
Best Local Similarity 43.4%; Pred. No. 2.9e-77;
Matches 249; Conservative 83; Mismatches 189; Indels 53; Gaps 9;

QY 20 PLGLPLSPGAL-----PRPA-----QAQDVVDLDFFTOEPLHLVSPS 55
Db 18 PPACIAPGALYIALLLHLSLSQAGDRPLPVDRAAGLKEKTLILLDVSTKNPVRTVNE 77

QY 56 FLSVTIDANLATDPRFLILLGSPKRLTLARGLSPAYLRFGGTKTDFLIF-----DPKKEST 111
Db 78 FLSLQLDPSIIHD-GWLDLFLSSKELVTLARGLSPAFRLFQGGKRTDFLQFQNLNPAKSRG 136

QY 112 FEERSYQSQVNQDI-----CKYGSIPDPVEEKLRLWPYQEQQL-LLREHYQK 158
Db 137 GPGPDYLLKNYEDDIVRSQVALDRQKQCKIAQ-HPDVMLELQREKAAQMHVLVLLKEQFSN 195

QY 159 KFKNSTYSRSSVDVLYTFANCSGDLIFGLNALLRTADLOWNSSNAQLLLDYCSSKGNYI 218
Db 196 TYSNLIITARSLLKLYNFADCSGLHLIFALNALRRPNNSWSSALSLLKYASKKNI 255

QY 219 SWELGNPNPSFLKKADIFINGSQLGEDIYIQLHKLRLK-STFKNAKLYGPDYQPPRKTK 277
Db 256 SWELGNPNNYRTMHWGRAVNGSQLGKDYIQLKSLQPIRIYSRASLYGNIGRPKKNVIA 315
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Job time : 237 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 27, 2006, 17:35:01 ; Search time 41 Seconds
(without alignments)
1274.285 Million cell updates/sec

Title: US-10-676-079-2

Perfect score: 2842
Sequence: 1 MLRSKPALPPPLMLLLGP.....LPAPSYFFVIRNAKVAACI 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	897.5	31.6	480	2 JC7506	heparanase protein
2	416	14.6	521	2 T45608	hypothetical prote
3	169.5	6.0	190	2 T01953	hypothetical prote
4	112.5	4.0	356	2 F64383	hypothetical prote
5	111.5	3.9	575	2 T12094	beta-fructofuranos
6	111	3.9	670	2 T10666	hypothetical prote
7	111	3.9	688	2 S32961	hypothetical prote
8	111	3.9	2298	2 T49648	hypothetical prote
9	109.5	3.9	879	2 E91031	probable outer mem
10	108.5	3.8	411	2 S74760	hypothetical prote
11	107.5	3.8	500	2 D87541	beta-xylosidase [i
12	106	3.7	879	2 F85875	probable fibrinoly
13	105	3.7	788	2 T38446	microtubule-associ
14	104.5	3.7	700	1 S00652	phosphoribosylamin
15	104	3.7	432	2 F70411	adenylosuccinate s
16	104	3.7	2013	2 A11489	probable peptidogl
17	103.5	3.6	587	2 S36231	beta-fructofuranos
18	103.5	3.6	676	2 AF1153	transcription anti
19	103.5	3.6	687	2 F85188	retrotransposon li
20	103	3.6	796	2 D97065	transketolase (imp
21	101	3.6	594	2 A82913	hypothetical prote
22	101	3.6	644	2 A97268	methionyl-tRNA syn
23	100.5	3.5	805	2 C86525	DNA gyrase subunit
24	100.5	3.5	805	2 H72098	DNA gyrase, chain
25	100.5	3.5	989	2 A82140	toxin secretion AB
26	99.5	3.5	510	2 H69893	conserved hypothet
27	99.5	3.5	837	1 A31842	endo-1,4-beta-xyla
28	99	3.5	897	2 G02529	dynein heavy chain
29	99	3.5	4644	1 A38905	dynein heavy chain

30	98.5	3.5	596	2 T04506	hypothetical prote
31	98.5	3.5	629	2 C64180	hypothetical prote
32	98.5	3.5	654	2 T14202	NADH2 dehydrogenas
33	98.5	3.5	699	2 F95146	DNA topoisomerase
34	98.5	3.5	701	2 D98014	DNA topoisomerase
35	98.5	3.5	746	2 T46821	siderophore recept
36	98.5	3.5	746	2 A95420	RhtA Rhizobactin r
37	98.5	3.5	1012	2 JC5925	membrane klotho pr
38	98	3.4	465	2 T19113	hypothetical prote
39	98	3.4	716	1 C60008	RNA-directed RNA p
40	98	3.4	760	2 T34414	hypothetical prote
41	98	3.4	817	2 H75035	probable membrane
42	97.5	3.4	454	2 T20829	probable serine ca
43	97.5	3.4	511	2 S61166	probable membrane
44	97.5	3.4	604	2 E75119	hypothetical prote
45	97.5	3.4	804	2 G71546	probable DNA gyras

ALIGNMENTS

RESULT 1
JC7506
heparanase protein 2a - human
C:Species: Homo sapiens (man)
C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C:Accession: JC7506
R:McKenzie, E.; Tyson, K.; Stamps, A.; Smith, P.; Turner, P.; Barry, R.; Hirccock, M.; i
Biochem. Biophys. Res. Commun. 276, 1170-1177, 2000
A:Title: Cloning and expression profiling of Hpa2, a novel mammalian heparanase family
A:Reference number: JC7506
A:Accession: JC7506
A:Molecule type: mRNA
A:Residues: 1-480 <MCK>
A:Cross-references: UNIPROT:Q9HB39; UNIPARC:UPI000003B88A; GB:AF282885
C:Comment: This protein, an intracellular membrane-bound enzyme, has biological and the
therapies.
C:Genetics:
A:Gene: hpa2a
A:Map position: 10q23-10q24
C:Keywords: heparin binding; membrane bound

Query Match 31.6%; Score 897.5; DB 2; Length 480;
Best Local Similarity 36.0%; Pred. No. 5.5e-59;
Matches 202; Conservative 74; Mismatches 146; Indels 139; Gaps 9;

Qy	20	PLGLSPGAL-----PRPA-----QAQDVVDLDFTEPELHLNPS	55
Db	18	PPACLAFGALYLALLHLSSQAQDRRPLFVDRAAGLKEKTLILLDVSTKPNVRTVNE	77
Qy	56	FLSVTIDANLATDPRFLLILGSPKRLTLARGLSPAYLRFPGTKTDFLIF----DPKKEST	111
Db	78	FLSLQLDPSIHD-GWLDLFSSKKLVTLARGLSPAFLRFPGTKRTDFLQFQNLRPAPKR-	135
Qy	112	FEERSYQSQVNQDICKYISPPDVEKRLWPYQEQQLLRLREHYKKFNSTYSRSVD	171
Db	136	-----CGPGPD-----YLLKNYE-----	148
Qy	172	VLYTFANCSGLDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNFSPFLK	231
Db	149	-----DEPNNYRT	156
Qy	232	KADIFINGSQIGDYIQLHKLRLK-STFKNAKLYGPDVGOPRRKTKAMKLSFLKAGEVI	290
Db	157	MHGRAVNGSQLGKDYIQLKSLQIPRIYSRSLYGPNIQPRKNVIALLDGFMKVGSTV	216
Qy	291	DSVTWHHYLNGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKKVWLGETSSAYGG	350
Db	217	DAVTWQHCYIDGRVWKVMDFLKTRLLDLSQDIRKIQKVNTYTPGKKIWLEGVVTTTSAG	276
Qy	351	GAPLLSTFPAGFWLKDGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSLFP	410
Db	277	GTNNLSDSYAAGFLWNLTLGLANQIGDVIIRHSFFDHGYNHLVDQNFNPLPDYWLSLFP	336

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Qy 411 KKLVTCKVLMAVSGSKER-----KLAVYLCTNTDPRYKEGDLTLVAINLHNV 461
Db 337 KRLIGPKVLAVHVAGLQKRPGRVIRDKLRIYAHCTNHHNNYVRGSGITFIILHRSR 396
Qy 462 KYLRPLPYFNSKNQVDKYLLRPLGPHGLLSKSVQLNGLTLKWVDDQTLPLMEKPLRPGSS 521
Db 397 KKIKLAGTLRDKLVHQLLYLQYPQGELSKSVQLNGQLPLWVDDGTLPELKFRLPRAGRT 456
Qy 522 LGLPAFYSFFVIRNAKVAAC 542
Db 457 LVIPPVMTGFFVKNVNALAC 477

RESULT 2
T45608
hypothetical protein F13G24.30 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45608
R:Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Ba
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23009
A:Accession: T45608
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-521 <BEV>
A:Cross-references: UNIPROT:Q9SDA1; UNIPARC:UPI00000A497C; EMBL:AL133421
A:Experimental source: cultivar Columbia; BAC clone F13G24
C:Genetics:
A:Map position: 5
A:Introns: 53/3; 66/1; 127/2; 177/1; 256/1; 319/2; 361/2; 394/3
A:Note: F13G24.30

Query Match 14.6%; Score 416; DB 2; Length 521;
Best Local Similarity 29.2%; Pred. No. 4.7e-23;
Matches 154; Conservative 68; Mismatches 184; Indels 122; Gaps 24;
Qy 75 LGSPKRLTARGLSPAYLRFGTGKTDFLIFPDKKESTPEERSYQSQVNDICKYGSIPP 134
Db 55 LTRPLLTKAIRAKFKPLRIRIGSLQDQVIYDGNLKT-----PCR----- 94
Qy 135 DVEEKLRLWEPQOEQLLREHYQKFKNS---TYSRSSV-----DVLVTEANCSDLILF 186
Db 95 -----PFQKM-----NSGLFGFSKGLCHMKRMDLNSFLTATGAVVTF 132
Qy 187 GLNALLRTADLQ-----WNSSNAQLLLDYCSSKGYNI-SWELGNPNPSFLKRAIDIPIN 238
Db 133 GLNALRGRHKLGRKAWGAWDHINTQDFLNTVTSKGYVIDSWFEGNELSG-SGVGASVS 190
Qy 239 GSQLGEDYIQLHKLRLKSTFNKALYGPDPVGPQ-----RRKTAKMLKSFLKAGGEVIDSV 293
Db 191 AELYKDLILVKDVINK-VYKNSWLHKPLVAPGGFYEQQWYTKLEI---SGPSVWDV 246
Qy 294 TWHYYLNGRT--ATREFLAPDVLIDIFISSVQKVP-----QVVESTRGKKVILGETSSA 347
Db 247 THHIYNLGSDNPALVKKIMDPS-----YLSQVSKTFFKDVNQTIQSHPWASPWVGESGA 302
Qy 348 YGGGAPLLSDTFAAGFMWLDKGLGSARMGIEVVMRQVFFGAGNYHLVDE-NPDPPLDYWL 406
Db 303 YNSGGRHVSDTDFIDSWYLDQLGMSARHNTKYVCHQTLVG-GFYGLLEKGTVPVNPDIYS 361
Qy 407 SLLFKKLVTGKVLMAVSGSKRRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYL-- 464
Db 362 ALLWHLRLMGKGLAVQTDGPP--QLRVVAHCSK-----GRAGVTLLILNLSNQSDFTVS 413
Qy 465 -----RLPYFES---NKQVDKYLRLP-----LGPHG--LLSKSVQL 495
Db 414 VSNGLNVNLVAESRKKSLDTLTKRPFWSMGSKASDGYLNRREYHLTPENGVLRSKTMWL 473
Qy 496 NGLTLRWVDDQTLPLMEKPLRP-GSSSLGLPAFYSFFVIRNAKVAAC 542
Db 474 NGKSLKPTATGDIPSL-EPVLRSVNSPLNVPLSLMSFVLPLNFDASAC 520
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```
RESULT 3
T01953
hypothetical protein T2L5.6 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01953
R:Geisel, C.; Smith, A.; Le, T.
submitted to the EMBL Data Library, October 1998
A:Description: The sequence of A. thaliana T2L5.
A:Reference number: Z14470
A:Accession: T01953
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-190 <GEI>
A:Cross-references: UNIPROT:O82604; UNIPARC:UPI00000A8F7D; EMBL:AF096371; NID:G3695386;
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Introns: 36/2; 69/3
A:Note: T2L5.6
C:Superfamily: Arabidopsis thaliana hypothetical protein T2L5.6

Query Match 6.0%; Score 169.5; DB 2; Length 190;
Best Local Similarity 27.8%; Pred. No. 2.3e-05;
Matches 54; Conservative 34; Mismatches 57; Indels 49; Gaps 9;
Qy 382 RQVFFGAGNYHLVD-ENFPDPLDYWLSLLFKKLVTGKVLMAVSGSKRRLRVYLHCTNT 440
Db 12 RQSLIG-GNYGLTNTFTPNPDYVSALIWQLMGRKALFTTFSGTK--KIRSYTHCA-- 66
Qy 441 DNPYKEGDLTLVAINLHV-----TKYLRLPYFPFSNKQVDKYLRLPL 483
Db 67 ---RQSKG-ITVLLMLNDNTTVVAKVELNNSFSRLHTKHKM-----SYKASSQLFG-- 115
Qy 484 GPHGLL-----SKSVQLNGLTLKWVDDQTLPLMEKPLRPGSSLGLPAFS 528
Db 116 GPNGVIOREEYHLTAKDGNLHLSQTMLNGLNALQVNSMGDLPPIEPIHINSTEPIIAPYS 175
Qy 529 YSFFVIRNAKVAAC 542
Db 176 IVFVHRNVVVPAC 189

RESULT 4
F64383
hypothetical protein MJ0670 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: F64383
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: F64383
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-356 <BU>
A:Cross-references: UNIPROT:Q58084; UNIPARC:UPI0000139BAF; GB:U67514; GB:L77117; NID:928
C:Genetics:
A:Map position: REV596956-595886
A:Start codon: GTG

Query Match 4.0%; Score 112.5; DB 2; Length 356;
Best Local Similarity 21.2%; Pred. No. 1.1; Mismatches 125; Gaps 18;
Matches 85; Conservative 48; Indels 143;
Qy 126 ICKY-----GSTPPDVEEKLRLWEPYQQLLREHYQKFKNSTYSRSSVD----- 171
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Db 14 IRKTMKLYNGKNEKDIKERLIKE-----LKEBHLVETEDGTGTYTLKADEEBEMHSHV 66
Qy 172 -----VLYTFANCGLDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNPE 226
Db 67 GALKEAIVKFAKPS-----KITDL-----SNPR-VLDLCSGMGYNATAALAHYK 109
Qy 227 NS-----FL-----KQADIFINGSQGEYDIQHLKLLRKSTF 258
Db 110 NAEIDMVEICEVFLFLFDLPYKEHEIINKVREYFLN--KITGIBY-----KSDY 159
Qy 259 KNAKLYGPDVGOPRRKTAKMLKSPFKAGGEVIDSVTWHYVYNGRTAT--REDFLNPDVL 316
Db 160 DNINLY---VGDARKFIKSDKKY-----NVFHDAPSPKRDPTLYTYDFL----- 202
Qy 317 DIFISSVQKVFQVVESTPRGKWLGETSAYGGGAPLLSDTFAAGFMWLDKLGSLARMG 376
Db 203 -----KEIYKRMEDN--GVLI-----SYSSAIPFERSALVDCGFVISEKESVGRKRG 246
Qy 377 IEVVMRQVFGAGNYHLVDENFD-----PLPDYWLSLFLFKLVGTQVLMASVQGSRRR 429
Db 247 ITLAYKNPNFKPNRINEVDERSVIALSPYRDETLSLTKDKIIEDREERREKLEKLI 306
Qy 430 KLRVYLHCTNTDNPYREGDLTLVA--INLHNTVKYLRLPY 468
Db 307 KIGKYLSTKQIKGNIPBEILKIQKEDLNSSEIILKQMLRF 347
RESULT 5
T12094
beta-fructofuranosidase (EC 3.2.1.26) - fava bean
C;Species: Vicia faba (fava bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12094
R;Weber, H.; Borisjuk, L.; Heim, U.; Buchner, P.; Wobus, U.
Plant Cell 7, 1835-1846, 1995
A;Title: Seed coat-associated invertases of Fava bean control both unloading and storage
A;Reference number: Z17416; MUID:96093423; PMID:8535137
A;Status: preliminary;
A;Accession: T12094
A;Molecule type: mRNA
A;Residues: 1-575 <WEB>
A;Cross-references: UNIPROT:Q43855; UNIPARC:UPI000009D74A; EMBL:Z35162; NID:9861154; PID
A;Experimental source: cv. Fribio, seed coat
C;Genetics:
C;Superfamily: beta-fructofuranosidase
C;Keywords: cell wall; glycoprotein; glycosidase; hydrolase
Query Match 3.9%; Score 111.5; DB 2; Length 575;
Best Local Similarity 21.4%; Pred. No. 2.6;
Matches 72; Conservative 48; Mismatches 107; Indels 109; Gaps 19;
Qy 46 QEPHLHVS-----PSFLSVTIDANLATDPRFLLILGSPKRLTLARGLS-----P 89
Db 228 KPIHSAKRTGMWECDFYFVSLGKNGLD--LSMMGNVNVKHLKNSLDITRYEYITG 285
Qy 90 AYLR-----FGTKTDF-----LIPDKKESTFEERSYV-----OSQVQ 124
Db 286 TYLQNDQKYPDKTSEDCWGLRYDYGNFVASKSFDPDK-----NRRITWGNESDTKE 341
Qy 125 DICKYG-----SIPPDV-----BEKLEWYQEQLLLR-----EHYQKFKNSTYRSV 170
Db 342 DDVKKGWAGIQAIPRTWLDSSRRQLR-QWPEELNLRGKQVEMKRLKKGY---L 396
Qy 171 DVLYTFANCGLDLIFGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNPNSFL 230
Db 397 EVKGITASQADVEVTFSSLDKAEAFDPNWNAAE---DLCAQKGSKVRGGV--PFGLL 451
Qy 231 KKADIFINGSQGEYDIQOL-----HKLL-----RKSTFKNAKLYGP-----DV 268
Db 452 TLA-----SKLEEYTSVFRFVKAAKHKILMCSDAKSSSLNRELYKPSFAGVNVLD 505
Qy 269 GOPRRKTAKMLKFLKAGGEVIDSVTWHYVYNGRT 304

Db 506 GNNKLSLRSL-----IDHSVVESFVGCGKT 531
RESULT 6
T10666
hypothetical protein F621.40 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10666
R;Bavan, M.; Lennard, N.; Quail, M.; Harris, B.; Bajandream, M.A.; Barrell, B.G.; Banci
submitted to the Protein Sequence Database, June 1999
A;Reference number: T16533
A;Accession: T10666
A;Molecule type: DNA
A;Residues: 1-670 <BBV>
A;Cross-references: UNIPROT:Q9M090; UNIPARC:UPI000004AF11; EMBL:AL049914; GSPDB:GN0006;
A;Experimental source: cultivar Columbia; BAC clone F621
C;Genetics:
A;Gene: ATSP:F6E21.40
A;Map position: 4
A;Introns: 47/3; 87/1; 123/3; 203/3; 230/2; 255/3; 284/3; 305/1; 335/3; 347/3; 370/3;
C;Superfamily: Schizosaccharomyces pombe negative regulator of mitosis skbl
Query Match 3.9%; Score 111; DB 2; Length 670;
Best Local Similarity 22.4%; Pred. No. 3.6;
Matches 123; Conservative 77; Mismatches 194; Indels 156; Gaps 33;
Qy 51 LVSPSFLSVTIDANLATDPRFLLILGSPKRLTLARGLSPAY--LRFGTDTDFLIDPK- 107
Db 47 LVDPYSRPSLVEGN-GVDTQVLPVCGSDLV-----LSPSQWSSHVVVGKISSWIDLSD 99
Qy 108 -----KESTFEERSYVQSOVNOQIDIKYGSIPDPVEKRLRWPYQBLRLREHYQKFK 161
Db 100 EVLRMDSSETLKQEIATWATHLSQME-----PD-----LTRPHYLAGGL 139
Qy 162 NSTYSRSSV-----DVLY-----TFANCS--GLDLIFGLNALLRTADLQWSSNAQLL 207
Db 140 RVSCRSSFTSDTFLYKITFNQALTFQGSLSFLCLNVALKWLRLVPLVK--SEGD 196
Qy 208 LDYCSSKGYNISWELGN-----EPNSFLKKA-DIFIN-----GSQGEDYIQLHKL 253
Db 197 DD--TSEGLNDSWELWNSFRLLCEHDSKLSVALDVLSTLPSETSLGRMMGES-VRAAIL 253
Qy 254 RKSTFKNAKLYGPDVGOP--RRKTAKMLKSF--KAGGEVIDSVTWHYVYNGRTATRED 310
Db 254 TDAFLTNAR-----GYPCLSKRHQKLIAGFFPHAAQVVICGKPVHMLQKPLDSSSGTE 307
Qy 311 LNPDVLDIFISSVQKVFQVVESTPRGKWLGETSAYGGGAPLLSDTFAAGFMWLDKLG 370
Db 308 KNP--LRIVLDYVAYLFQKWSLSEQRTELGYRDFLQAPLQPLMDNLEAQTETPE--- 362
Qy 371 LSARMGIEVVMRQVFGAGNYHLVDENFDPLPDYWLSSLFKKLVGTQVLM----- 420
Db 363 ---RDSVKYIQYQ---RAVEKALVDR---VPDEKASEL-----TTVLVVGAGRGPLV 406
Qy 421 -ASVQGSKR--RKLRVYLHCTNTDNPYREGDLTLVAINLHNTK-----YLRLPY 468
Db 407 RASLQAAETDRKLYV---AVEKNPN-----AVVTLHNLVQMEGVEDVTIISCDM 455
Qy 469 PFSN--KQVDKYLLRPLGPHGLLSKSVQLNGLTLKMWDDQDTLPPLM---EKPLRPGSSLG 523
Db 456 RFWNAPEQADILVSELGSGF-----DNELSPEDLGAQRFLKP-DGIS 498
Qy 524 LPAFSYSPFFV 533
Db 499 IPS-SYTSFI 507
RESULT 7
S32961
hypothetical protein YBR259w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR1727

A;Experimental source: strain 972h-; cosmid c405

C;Genetics:

A;Gene: ADE1; SPDB:SPBC405.01

A;Map position: 2

C;Superfamily: Saccharomyces cerevisiae ADE5 multifunctional protein; phosphoribosylamin

C;Keywords: cyclo-ligase; purine nucleotide biosynthesis

F;5-425/Domain: phosphoribosylamine-glycine ligase homology <PGL>

F;439-767/Domain: phosphoribosylformylglycinamide cyclo-ligase homology <PFCL>

Query Match 3.7%; Score 104.5; DB 1; Length 788;

Best Local Similarity 27.7%; Pred. No. 14;

Matches 70; Conservative 36; Mismatches 114; Indels 33; Gaps 11;

Qy 297 HYLYNGRTATRE--DFLNPV-LDIFISSVQKVVVEST-RPGKVMLETSSAY---- 348

Db 424 HHALNPKRKTRITLYENSGVSVVDNEFVQRIKDLVKSTRPGADADIGFGGIFDLK 483

Qy 349 -GGGAPLL-SDTFAAGFWLKDGLSAR--MGIEVMRQVPPFGAGNTHLVDFDPL--P 402

Db 484 AGMNDPLLVSATDGVGSKLLIALSLNKHDTVGDIDVAMNV-----NDLVVQGAERLIFL 537

Qy 403 DYWLSSLFLKLVGKVLMAVQSGSKRRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTK 462

Db 538 DYFATGSLDLKVSFVEGVVKGCKQAGCALVGGETSEMPGLYHDHYDANGTSVGAVSR 597

Qy 463 YLRLPYPPFSNKKQVDKYLRLPLGPHGLLSKVSQNLGLTL--KMVD----DOTLPPLMEKPL 516

Db 598 DDILPKPESFSGDILL-----GLASDGVHSGYSLVRKIVEYSDLEVTSCPMDKNV 650

Qy 517 RPSGSLGLPAFSY 529

Db 651 RLGDSLIIPRIY 663

RESULT 15

F70411

adenylosuccinate synthetase - Aquifex aeolicus

C;Species: Aquifex aeolicus

C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C;Accession: F70411

R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov

V. Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A;Reference number: A70300; MUID:98196666; PMID:9537320

A;Accession: F70411

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-432 <AAQF>

A;Cross-references: UNIPROT:O67321; UNIPARC:UPI00000565A2; GB:AE000733; NID:g2983720; PT

A;Experimental source: strain VF5

C;Genetics:

A;Gene: pura

C;Superfamily: adenylosuccinate synthase

Query Match

Best Local Similarity 3.7%; Score 104; DB 2; Length 432;

Matches 96; Conservative 39; Mismatches 128; Indels 138; Gaps 22;

Qy 15 LLLGLPLGSPGALPRPAQADVVLDL-----FFTQEPHLHVSPS 55

Db 51 ILHLLPTGILHEHVKGVIAGM-VVDLEVLHKEVKNEEKGIYVKERLFIISRAHLVMPY 109

Qy 56 FLSTVIDANLATDFRLLILGSPK--LRTLARGLSPAYL-RFGTKTDFLIFDPKKESTF 112

Db 110 H-----KLLDSLFEKKKGIGTTLRGIGPAYMPKYG--RKGIRISDLKDKRF 154

Qy 113 EERSYQSOVNODICKYGIIPDVEEK-----LRLEWVQEOQLLREHYQKKFKNSTY 165

Db 155 ----YTLLEDNLDVFK-----NICEKVFCEKFDLDINOIYEEQL-----RYFEFKENV- 199

Qy 166 SRSSVDVLYTFANGSGLDLIFGLNALRTADL-----QWNSNAQLLDYCSSKGYNISWE 221

Db 200 -----VDLLRFFNTQKGSVLFEAGAGTLLDVMGTYPYVTSNASAL-----GLSNG 246

Qy 222 LGNEPNSFLKKADIFING-----SQL-GEDYIQLHKLRLKSTFKNAKLYG 265

Db 247 TGMPPKYF---SDAFFLGVAKAYTRVGEOPFFTELKGESEKRLREL-----GGEYG 295

Qy 266 PDVGQPRR---KTAKMKSLKAGGEVIDSVTWHYHLYNGRTATREDFLNP----- 313

Db 296 STTGRPRRCGWLDLVALKYAVQVNG-----LDGFVITKLDVLDTFDEVKVCVA 343

Qy 314 -----DVLDFISSVQKVFQV--VESTRPKKVMLETSSA 347

Db 344 YELDGEVIDYFPASYSSELIRKVPYKTLKG---WKKSTKGA 381

Search completed: February 27, 2006, 17:39:32

Job time : 44 secs

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Result No.	Query	Score	Match	Length	DB	ID	Description
1	1721	100.0	1721	6	CQ840766	Sequence	
2	1721	100.0	1721	6	CQ840768	Sequence	
3	1721	100.0	1721	6	CQ840858	Sequence	
4	1721	100.0	1721	6	CQ840860	Sequence	
5	1721	100.0	1721	6	CQ971643	Sequence	
6	1721	100.0	1721	6	CQ971645	Sequence	
7	1719.4	99.9	1721	6	AR080679	Sequence	
8	1719.4	99.9	1721	6	AR080680	Sequence	
9	1719.4	99.9	1721	6	AR125603	Sequence	
10	1719.4	99.9	1721	6	AR125604	Sequence	
11	1719.4	99.9	1721	6	BD074427	Polynucleotide	
12	1719.4	99.9	1721	6	BD074428	Polynucleotide	
13	1719.4	99.9	1721	6	BD193236	Heparanase	
14	1719.4	99.9	1721	6	BD193237	Heparanase	
15	1719.4	99.9	1721	6	BD205238	Cells gene	
16	1719.4	99.9	1721	6	BD205239	Cells gene	
17	1719.4	99.9	1721	6	AR194189	Sequence	
18	1719.4	99.9	1721	6	AR194190	Sequence	

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QY 181 ACCTGGACTTCTTCAACCAGGAGCGCTGCACCTGGTGGAGCCCTCGTTCCTGTCGTC 240
Db 181 ACCTGGACTTCTTCAACCAGGAGCGCTGCACCTGGTGGAGCCCTCGTTCCTGTCGTC 240
QY 241 CCATTGACGCCAACCCTGGCCACAGGACCGCGGTTCTCATCTCTCTGGGTTCTCCAAAGC 300
Db 241 CCATTGACGCCAACCCTGGCCACAGGACCGCGGTTCTCATCTCTCTGGGTTCTCCAAAGC 300
QY 301 TTCTGACCTTGGCCAGAGGCTTGTCTCTCTGGTACCTGAGCTTTGGTGCCACCAAGACAG 360
Db 301 TTCTGACCTTGGCCAGAGGCTTGTCTCTCTGGTACCTGAGCTTTGGTGCCACCAAGACAG 360
QY 361 ACTTCTCTAAATTTTCGATCCCAGAGGAATCAACCTTTTGAAGAGAGAGTTACTGGCAAT 420
Db 361 ACTTCTCTAAATTTTCGATCCCAGAGGAATCAACCTTTTGAAGAGAGAGTTACTGGCAAT 420
QY 421 CTCAGTCAACAGGATATTTGCAAAATATGATTCATCCCTCTCTGATGTGAGAGAGT 480
Db 421 CTCAGTCAACAGGATATTTGCAAAATATGATTCATCCCTCTCTGATGTGAGAGAGT 480
QY 481 TACGTTTGGAAATGSCCTTACCAGGACAAATTCCTACTCCGAGAACACTTACCAGAAAAGT 540
Db 481 TACGTTTGGAAATGSCCTTACCAGGACAAATTCCTACTCCGAGAACACTTACCAGAAAAGT 540
QY 541 TCAAGAACAGCACCTTACTCAAGAAAGCTCTGTAGATGTCTATACTTTTGCAAACTGCT 600
Db 541 TCAAGAACAGCACCTTACTCAAGAAAGCTCTGTAGATGTCTATACTTTTGCAAACTGCT 600
QY 601 CAGGACTGGAATTGATCTTTGGCTTAAATGCGTTATTAAAGAACAGCAGATTGCGAGTGA 660
Db 601 CAGGACTGGAATTGATCTTTGGCTTAAATGCGTTATTAAAGAACAGCAGATTGCGAGTGA 660
QY 661 ACAGTTCTAAATGCTCAGTTCCTCTGGACTACTGCTTCTCCAGGGGTATTAACATTTCTT 720
Db 661 ACAGTTCTAAATGCTCAGTTCCTCTGGACTACTGCTTCTCCAGGGGTATTAACATTTCTT 720
QY 721 GGGAACTAGGCAATGAACCTAACAGTTTCCTTAAAGAGCGTGATATTTCATCAATGGGT 780
Db 721 GGGAACTAGGCAATGAACCTAACAGTTTCCTTAAAGAGCGTGATATTTCATCAATGGGT 780
QY 781 CGCAGTTAGGAGAGATTTTATCAATTGCAATAAACTTCTAAGAAAGTCCACCTTCAAAA 840
Db 781 CGCAGTTAGGAGAGATTTTATCAATTGCAATAAACTTCTAAGAAAGTCCACCTTCAAAA 840
QY 841 ATGCAAAACTCTATGCTCTGATCTTGGTACGCTCGAAGAACCGCTAAGATGCTGA 900
Db 841 ATGCAAAACTCTATGCTCTGATCTTGGTACGCTCGAAGAACCGCTAAGATGCTGA 900
QY 901 AGAGCTTCTCAAGGCTGGTGGAGAGTGATTTGATTACATGTCATGCTACTATT 960
Db 901 AGAGCTTCTCAAGGCTGGTGGAGAGTGATTTGATTACATGTCATGCTACTATT 960
QY 961 TGAATGAGCGACTGTACACGGAAGATTTTCTAAACCCTGATGATTTGACATTTT 1020
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QY 1021 TTTTCATCTGTGCAAAAAGTTTTCAGTGGTTTGAGACACACGCGCTGGCAGAGTCT 1080
Db 1021 TTTTCATCTGTGCAAAAAGTTTTCAGTGGTTTGAGACACACGCGCTGGCAGAGTCT 1080
QY 1081 GGTTAGGAGAAAACAGCTCTCATATGAGGCGGAGCGCCCTTCTATCCGACACCTTTG 1140
Db 1081 GGTTAGGAGAAAACAGCTCTCATATGAGGCGGAGCGCCCTTCTATCCGACACCTTTG 1140
QY 1141 CAGCTGGCTTTATGTGGCTGATAAATTTGGCCCTGTTCAGCCCGAATGGGAATAGAGTGG 1200
Db 1141 CAGCTGGCTTTATGTGGCTGATAAATTTGGCCCTGTTCAGCCCGAATGGGAATAGAGTGG 1200
QY 1201 TGATGAGGCAAGTATTTCTTTGAGCAGGAACCTACCAATTTAGTGGATGAAACTTCATC 1260
Db 1201 TGATGAGGCAAGTATTTCTTTGAGCAGGAACCTACCAATTTAGTGGATGAAACTTCATC 1260
QY 1261 CTTTACCTGATTAATTGGCTATCTCTCTGTTCAAGAAAATGGTGGGCCAACCAAGGTGTA 1320
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Db 1261 CTTTACCTGATTAATTGGCTATCTCTCTGTTCAAGAAAATGGTGGGCCAACCAAGGTGTA 1320
QY 1321 TGGCAAGCGTGCAAGGTTCAAAGAGAAAGAGCTTCGAGTATACCTTCATTGCAACAACA 1380
Db 1321 TGGCAAGCGTGCAAGGTTCAAAGAGAAAGAGCTTCGAGTATACCTTCATTGCAACAACA 1380
QY 1381 CTGACAAATCCAAGGTATAAAGAGAGGAGATTAACTCTGTATGCCATAAATCCTCATACG 1440
Db 1381 CTGACAAATCCAAGGTATAAAGAGAGGAGATTAACTCTGTATGCCATAAATCCTCATACG 1440
QY 1441 TCACCAAGTACTTTCGCGGTATACCTTATCTCTTTCTAAACAAGCAAGTGGATAAATACCTTC 1500
Db 1441 TCACCAAGTACTTTCGCGGTATACCTTATCTCTTTCTAAACAAGCAAGTGGATAAATACCTTC 1500
QY 1501 TAAGACCTTTGGGACCTCATGGATTACTTTTCCAAAATCTGTCCAACTCAATGGTCTAACTC 1560
Db 1501 TAAGACCTTTGGGACCTCATGGATTACTTTTCCAAAATCTGTCCAACTCAATGGTCTAACTC 1560
QY 1561 TAAAGATGGTGGATGATCAAAACCTTGCACCTTTAATGGAAGAAACCTCTCCGGCCAGGAA 1620
Db 1561 TAAAGATGGTGGATGATCAAAACCTTGCACCTTTAATGGAAGAAACCTCTCCGGCCAGGAA 1620
QY 1621 GTTCACCTGGCTGCCAGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680
Db 1621 GTTCACCTGGCTGCCAGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680
QY 1681 CTGCTTGCATCTGAAATAAATAATATACTAGTCTCGACACTG 1721
Db 1681 CTGCTTGCATCTGAAATAAATAATATACTAGTCTCGACACTG 1721

RESULT 2
CQ840768 LOCUS CQ840768 1721 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 11 from Patent EP1439193.
ACCESSION CQ840768
VERSION CQ840768.1 GI:50838371
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Pecker, I., Vlodavsky, I. and Feinstein, E.
TITLE Antibody directed to polypeptide having heparanase activity
JOURNAL Patent: EP 1439193-A 11 21-JUL-2004;
Insight Biopharmaceuticals Ltd. (IL); HADASIT MEDICAL RESEARCH
SERVICES AND DEVELOPMENT LTD. (IL)
FEATURES
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Query Match 100.0%; Score 1721; DB 6; Length 1721;

Query Match	100.0%;	Score 1721;	DB 6;	Length 1721;
Best Local Similarity	100.0%;	Pred. No. 0;		
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Db	61	AGATGCTGCTGCGCTCGAAGCCTCGCTGCGCGCGCGCTGATGCTGCTGCTCTCTGGGGC	120	
Qy	121	CGTGGGTGCCCTCTCCCTGGCGCCCTGCGCCGACCTGGCGAAGCACAAGACAGTCTGTG	180	
Db	121	CGTGGGTGCCCTCTCCCTGGCGCCCTGCGCCGACCTGGCGAAGCACAAGACAGTCTGTG	180	
Qy	181	ACCTGGACTTCTTACACGAGGCGGCTGCACCTGGTGAGCCCTCGTTCTCTGTCCGTCA	240	
Db	181	ACCTGGACTTCTTACACGAGGCGGCTGCACCTGGTGAGCCCTCGTTCTCTGTCCGTCA	240	
Qy	241	CCATTGACGCCAACCTGGCCACGACCGCGGTTCTCATCTCTCGGTTCTCCTCAAGC	300	
Db	241	CCATTGACGCCAACCTGGCCACGACCGCGGTTCTCATCTCTCGGTTCTCCTCAAGC	300	
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Db	301	TTGCTACTTTGGCCAGAGGCTTGCTCTCGCTACCTGAGGTTTGGTGCCACCAAGACAG	360	
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ORIGIN

Query Match 100.0%; Score 1721; DB 6; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 CGCTGGCTCCCTCTCCCTGGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCG 180

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Db 181 ACCTGGACTTCTTCACCAGAGCGCTGCACTGGTGAGCCCTCGTCTCTGTCCTGCTCA 240

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RESULT 5

CQ971643
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CQ971643
Sequence 9 from Patent EP1489183.
CQ971643
CQ971643.1
GI:57163124
Homo sapiens (human)
Homo sapiens

1721 bp
DNA
linear
PAT 05-JAN-2005

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Pecker, I., Vlodavsky, I. and Feinstein, E.
TITLE Polynucleotide encoding a polypeptide having heparanase activity and expression of same in transduced cells
JOURNAL Patent: EP 1489183-A 9 22-DEC-2004;
Insight Biopharmaceuticals Ltd. (IL); HADASIT MEDICAL RESEARCH SERVICES AND Development Ltd. (IL)
Location/Qualifiers 1. .1721

FEATURES

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ORIGIN

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Best Local Similarity	100.0%;	Pred. No. 0;		
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Qy	661	ACAGTTCTTAATGCTCAGTGTCTCTGGACTACTGCTCTTCCAAAGGGGTATAAATTTCTT	720	
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RESULT 6

CO971645 LOCUS 1721 bp DNA linear PAT 05-JAN-2005
DEFINITION Sequence 11 from Patent EP1489183.
ACCESSION CO971645
VERSION CO971645.1 GI:57163125
KEYWORDS Homo sapiens (human)
SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE Pecker, I., Vlodavsky, I. and Feinstein, E.
AUTHORS Polynucleotide encoding a polypeptide having heparanase activity
TITLE and expression of same in transduced cells
JOURNAL Patent: EP 1489183-A 11 22-DEC-2004;
Insight Biopharmaceuticals Ltd. (IL); HADASIT MEDICAL RESEARCH
SERVICES And Development Ltd. (IL)
FEATURES Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 1721; DB 6; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAGAGCTTTGACTCTCCGCTGCGCGGACGCTGGCGGGGGAGCAGCCAGGTGAGCCCA 60
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Qy 1141 CAGCTGGCTTTATGCTGGGATAAAATTTGGGCTGTGAGCGGAGTGGGAATAGAAGTGG 1200
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Db 1681 CTGCTTGATCTGAATAAATAATATATAGTCTGACACTG 1721

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LOCUS Sequence 9 from patent US 5968822.
DEFINITION AR080679
ACCESSION AR080679
VERSION AR080679.1 GI:10007409
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1721)
AUTHORS Pecker, I., Vlodaysky, I. and Feinstein, E.
TITLE Polynucleotide encoding a polypeptide having heparanase activity
JOURNAL and expression of same in transduced cells
Patent: US 5968822-A 9 19-OCT-1999;
FEATURES Location/Qualifiers
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source /organism="unknown"
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Query Match 99.9%; Score 1719.4; DB 6; Length 1721;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1681 CTGCTTGATCTGAAATAAATAATATATAGTCTGACACTG 1721


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RESULT 9
LOCUS AR125603 1721 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6177545.
ACCESSION AR125603
VERSION AR125603.1 GI:14111665
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1721)
AUTHORS Pecker, I., Vlodavsky, I., Friedman, Y. and Perets, T.
TITLE Heparanase specific molecular probes and their use in research and
medical applications
JOURNAL Patent: US 6177545-A 1 23-JAN-2001;
FEATURES Location/Qualifiers
source 1..1721
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ORIGIN
Query Match 99.9%; Score 1719.4; DB 6; Length 1721;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTAGAGCTTTTCGACTCTCCGCTGCGCGAGCTGCGGGGGGAGCAGCCAGGTGAGCCCA 60
Db 1 CTAGAGCTTTTCGACTCTCCGCTGCGCGAGCTGCGGGGGGAGCAGCCAGGTGAGCCCA 60

Qy 61 AGATGCTGCTGCGCTCGAAGCTGCGTGC CGCGCGCGCTGATGCTGCTCTCTGGGGC 120
Db 61 AGATGCTGCTGCGCTCGAAGCTGCGTGC CGCGCGCGCTGATGCTGCTCTCTGGGGC 120

Qy 121 CGCTGGGTCCCTCTCCCTGGCGCCCTGCGCCGACCTGCGCAAGCAGAGAGCTCGTGG 180
Db 121 CGCTGGGTCCCTCTCCCTGGCGCCCTGCGCCGACCTGCGCAAGCAGAGAGCTCGTGG 180

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AR125604
LOCUS

DEFINITION Sequence 3 from patent US 6177545.
1721 bp DNA linear PAT 16-MAY-2001

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Qy 841 ATGCAAAACCTATGTCCTGATGTTGGTTCAGCTCGAAGAAAGACGGCTAAGATGCTGA 900
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SOURCE	unidentified
ORGANISM	unidentified
REFERENCE	unclassified.
AUTHORS	Pecker, I., Vladavsky, I. and Elena, F.
TITLE	Polynucleotide encoding polypeptide having heparanase activity and expression of the polypeptide in induced cell
JOURNAL	Patent: JP 2001514855-A 8 18-SEP-2001; INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES & DEVELOPMENT LTD
COMMENT	OS Nucleic acid PN JP 2001514855-A/8 PD 18-SEP-2001 PF 31-AUG-1998 JP 2000508806 PR 02-SEP-1997 US 08/922170, 02-JUL-1998 US 09/109386 PI IRIS PECKER, ISRAEL VLODAVSKY, FEINSTEIN ELENA PC C12N15/09, A61K38/00, A61P17/00, A61P29/00, A61P35/00, PC A61P37/00, PC A61P43/00, C12N5/10, C12N9/24, C12Q1/68, G01N33/15, G01N33/50// PO A61K39/395, PC A61K39/395, C12N15/00, A61K37/02, C12N5/00 CC Polynucleotide encoding polypeptide having heparanase activity and CC expression of the polypeptide in induced cell FH Key
FEATURES	Location/Qualifiers FT source 1..1721 /organism='Nucleic acid'. FT Location/Qualifiers 1..1721 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"
ORIGIN	Query Match 99.9%; Score 1719.4; DB 6; Length 1721; Best Local Similarity 99.9%; Pred. No. 0; Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	1 CTAGAGCTTTTCGACTTCCCGTCGGCGGCAGCTGGCGGGGGAGCACCAGGTGAGCCCA 60
Dd	1 CTAGAGCTTTTCGACTTCCCGTCGGCGGCAGCTGGCGGGGGAGCACCAGGTGAGCCCA 60
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Dd	181 ACCTGSAGCTTCTTCACCGAGGAGCGGTGCACCTGGTAGGCCCTGTTCTGTCCTGCTCA 240
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Dd	241 CCATTGAGCCAACTGSCCAGCAGCAGCGGGTTTCCTCATCTCTCGGTTCTCCAAGC 300
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Dd	301 TTCGTACTCTGGCCAGAGGCTTGTTCTCTGCGTACCTGAGGTTTTGGTGCCACCAAGACAG 360
Qy	361 ACTTCCATAATTTTCGATCCAGAGAAGATCACTTTGAAGAGAGAAGTTACTGGCAAT 420
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Qy	421 CTCAAAGTCAACAGGATATTTGAAAATATGATCCATCCCTCCTGATGTGGAGGAGAAGT 480
Dd	421 CTCAAAGTCAACAGGATATTTGAAAATATGATCCATCCCTCCTGATGTGGAGGAGAAGT 480
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BD193236			
LOCUS			
DEFINITION	BD193236	1721 bp	DNA linear PAT 17-JUL-2003
Heparanase specific molecular probes and their use in research and medical applications.			
ACCESSION	BD193236		
VERSION	BD193236.1	GI:33002975	
KEYWORDS	JP 2002512533-A/1.		
SOURCE	Streptococcus equi		
ORGANISM	Streptococcus equi		
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.			
REFERENCE	1	(bases 1 to 1721)	
AUTHORS	Pecker, I., Vlodavsky, I., Friedman, Y. and Perets, T.		
TITLE	Heparanase specific molecular probes and their use in research and medical applications		
JOURNAL	Patent: JP 2002512533-A 1 23-APR-2002;		
INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES & DEVELOPMENT LTD			
COMMENT	PN JP 2002512533-A/1		
PD 23-APR-2002			
PF 29-APR-1999 JP 1999555528			
PR 01-MAY-1998 US 09/071739			
PI IRIS PECKER, ISRAEL VLodaySKY, Yael FRIEDMAN, TUVIA PERETS PC			
C07K16/00, C07K16/40, G01N33/53, C07H21/02, C7H21/04, A61K39/395 CC			
nucleic acid			
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Db	1	CTAGAGCTTTTCGACTCTCCGCTGGCGGACGCTGGCGGGGGAGCAGCCAGGTGAGCCCA	60
Qy	61	AGATGCTGCTGGCTCGAAGCTGGCTGGCGCGCGCGCTGATGCTGCTCTCTGGGGC	120
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medical applications.
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VERSION BD193237.1 GI:33002976
KEYWORDS JP 2002512533-A/2.
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ORGANISM Streptococcus equi
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Pecker, I., Vlodavsky, I., Friedman, Y. and Perets, T.
Heparanase specific molecular probes and their use in research and
medical applications
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& DEVELOPMENT LTD
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BD205238
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DEFINITION Cells genetically modified for expressing recombinant heparanase
and method, and method of purifying recombinant heparanase.
ACCESSION BD205238
VERSION BD205238.1 GI:33015008
KEYWORDS JP 2002513560-A/1.
SOURCE unidentified
ORGANISM unclassified.
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AUTHORS Artzi,H.B., Herzhkovitz,M.A., Zeevi,O.Y., Pecker,I., Peleg,Y.,
Shlomi,Y., Moskowitz,H., Miron,D., Gilboa,A. and Mimon,M.
TITLE Cells genetically modified for expressing recombinant heparanase
and method, and method of purifying recombinant heparanase
JOURNAL Patent: JP 2002513560-A 1 14-MAY-2002;
INSIGHT STRATEGY AND MARKETING LTD
COMMENT OS Unidentified
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PD 14-MAY-2002
PF 29-APR-1999 JP 2000547200
PR 01-MAY-1998 US 09/071618,02-MAR-1999 US 09/260038 PI
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2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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42	97	3.4	726	2	G91237
43	97	3.4	760	2	T34414
44	96.5	3.4	510	2	H69893
45	96.5	3.4	621	2	A95250

ALIGNMENTS

RESULT 1

JC7506
heparanase protein 2a - human
C:Species: Homo sapiens (man)
C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C:Accession: JC7506
R:McKenzie, E.; Tyson, K.; Stamps, A.; Smith, P.; Turner, P.; Barry, R.; Hircock, M.; F
Biochem. Biophys. Res. Commun. 276, 1170-1177, 2000
A:Title: Cloning and expression profiling of Hpa2, a novel mammalian heparanase family
A:Reference number: JC7506
A:Accession: JC7506
A:Molecule type: mRNA
A:Residues: 1-480 <MCK>
A:Cross-references: UNIPROT:Q9HB39, UNIPARC:UPI000003888A, GB:AF282885
C:Comment: This protein, an intracellular membrane-bound enzyme, has biological and ther
therapies.
C:Genetics:
A:Gene: hpa2a
A:Map position: 10q23-10q24
C:Keywords: heparin binding; membrane bound

Query Match	31.5%	Score	893.5	DB 2	Length	480
Best Local Similarity	35.8%	Pred. No.	8.2e-59			
Matches	201	Conservative	75	Mismatches	146	Indels 139; Gaps 9
Qy	20	PLGLSPGAL	-----PRPA-----	QAQDVVDLDF	FTQEPHLVSPS	55
Db	18	PPACLAPGALY	LALLHLSSQAGDRRPLPVDRAAGLKEKTLILLDVSTKNPVRTNEN	77		
Qy	56	FLSVTIDANLATDPR	ELLILGSPKRLTARGLSPAVLFCGTTDFLIF	---DPKKEST	111	
Db	78	FLSLQDPSIIHD	-GWLDFLSSKRLVTLAGLSPAFLRFGGKRTDFLQFNLRNPAKSR	-135		
Qy	112	FEERSYQSQVNQDICKY	GISPPDVEEKLREWPYQEQILLRHHYQKFKKNSTYSSRSD	171		
Db	136	-----GPGPD-----	-----YLLKNYE-----	148		
Qy	172	VLYTFANCGLDLIF	IGLNALLRTADLQWSSNAQLLLDYCSSKGYNISWELGNEPNSFLK	231		
Db	149	-----	-----DEPNYRT	156		
Qy	232	KADIFINGSOLGEDFT	QLHKLK-STFKNAKLYGPDVGPORPKRTAKMLKSLFKAGEVI	290		
Db	157	MHGRAVNSQLGKDY	QLKSLQLPIRYGRASLYGNIPRKNVKTALLDGFMKVGSTV	216		
Qy	291	DSVTWHYHLYNGRTAT	RPNLDVLDIFITSSVQKVQVVESTRPGKVKWLGETSSAYGG	350		
Db	217	DATWQHCHIDGRV	KVMDFLTKRLDTSQIRKTKQVNTYTPGKKIWLGVVTSAG	276		
Qy	351	GAPLLSDTFAAGPM	WLDKGLSARMGIEVVMQVFFGAGNYHLVDENFDPLPDYWLSLLF	410		
Db	277	GTNNLSDSVAAGFL	WLTLMLANQGDIVVIRHSFEDHGYNHLVDQNFNPLPDYWLSLLY	336		

Qy 411 KKLVGTVKVLMAVSGSKRR-----KLRVYLCTNTDTPRYKEGDLTIYAINLHNT 461
Db 337 KRLTIGPKVLAVHVGAGLQKRPGRVIRDKLRIYAHCTNNHNNYVSGSITLFIINLHRSR 396
Qy 462 KYLRPLYPFNSKNQVDKYLRLPLGPHGLSKSVQLNGLTKMVDQDTLPPLMEKPLRPGSS 521
Db 397 KKIKLAGTLRDKLVHLYLQPYGQGLKSKSVQLNGQLPLVWDDGTLPELKPRPLRAGRT 456
Qy 522 LGLPAFYSFPIVIRNAKVAAC 542
Db 457 LVIPPVMTGMFVVKVNALAC 477
RESULT 2
T45608
hypothetical protein F13G24.30 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45608
R:Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Ba
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23009
A:Accession: T45608
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-521 <BEV>
A:Cross-references: UNIPROT:Q9SDAI; UNIPARC:UPI00000A497C; EMBL:AL133421
A:Experimental source: cultivar Columbia; BAC clone F13G24
C:Genetics:
A:Map position: 5
A:Introns: 53/3; 66/1; 127/2; 177/1; 256/1; 319/2; 361/2; 394/3
A:Note: F13G24.30
Query Match 14.7%; Score 417; DB 2; Length 521;
Best Local Similarity 29.2%; Pred. No. 3.4e-23;
Matches 154; Conservative 68; Mismatches 184; Indels 122; Gaps 24;
Qy 75 LGSPLKRLTARGLSPAYLRFQGTWDTFLIFPKKKESTFEERSYQSQVNDICKYGSIPP 134
Db 55 LTRPLLTAKIKAFKPLRIRIGSLQDQVIYDGNLKT-----PCR----- 94
Qy 135 DVEEKLRLWEPYQOQLLREHYQKFKNS---TYSRSV-----DVLTYFRANCSGLDLIF 186
Db 95 -----PFQKM-----NSGLFGFSKGLCHMKRWDELNSFLTATGAVVTF 132
Qy 187 GLNALLRTADLQ-----WNSSNAQLLLDYCCSKGYNI-SWELGNFPNSFLKKAIPIN 238
Db 133 GLNALRGHKLGRKAWGGAWDHINTQDFLNTVSKGYVIDSWERGNELSG--SGVGASVS 190
Qy 239 GSQIGEDFIQLHKLKRSFTFNKALYGPVQGP-----RRKTAKWLKSLFKAGGEVIDSV 293
Db 191 AELYGKDLILVKDINK-VYKNSWLHKPLVAPGFGVEQWYTKLLEI---SGPSVVDVV 246
Qy 294 TWHYYLNGRT--ATREDFLNPVDLDTFISSQKVF-----QVVESTPGKKVWGETSSA 347
Db 247 THHTYNLGSGNDPALVKKIMDPS-----YLSQVSKTFKDVNQTIQBHGFWASPWVSGSGA 302
Qy 348 YGGGAPLISDTFAAGFMWLDKGLSARMIWVRQFFGAGNYHLVDE-NFDPLPDYWL 406
Db 303 YNSGRHVSDTDFIDSFVWLDQLGMSARHNTKVYCRQTLVG-GFYGLLEKGTFFVNPDIYS 361
Qy 407 SLLPKFLVGTKVLMAVSGSKRRKRLRVYLHCTNTDNPYKEGDLTIYAINLHNTKYL-- 464
Db 362 ALLWHLRMKGVLAVQTDGPP--QLRVYAHCSK-----GRAGVTLLILLNSQSDFTVS 413
Qy 465 -----RLPYPPS---NKQVDKYLRLP-----LPGHG---LLSKSVQL 495
Db 414 VNSGINVVLNAESRKKSLDLTLRPFPSWIGSKASDGYLNREYHLTPENGVLRSKTMVL 473
Qy 496 NGLTKMVDQDTLPPLMEKPLRP--GSSIGLPAFYSFPIVIRNAKVAAC 542
Db 474 NGKSLKPTATGDIPLS-LPVLRSVNSPLNVLPLMSFIVLPNFDASAC 520

RESULT 3
T01953
hypothetical protein T2L5.6 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01953
R:Geisel, C.; Smith, A.; Le, T.
submitted to the EMBL Data Library, October 1998
A:Description: The sequence of A. thaliana T2L5.
A:Reference number: Z14470
A:Accession: T01953
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-190 <GEI>
A:Cross-references: UNIPROT:O82604; UNIPARC:UPI00000A08F7D; EMBL:AF096371; NID:g3695386;
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Introns: 36/2; 69/3
A:Note: T2L5.6
C:Superfamily: Arabidopsis thaliana hypothetical protein T2L5.6
Query Match 6.0%; Score 169.5; DB 2; Length 190;
Best Local Similarity 27.8%; Pred. No. 2.2e-05;
Matches 54; Conservative 34; Mismatches 57; Indels 49; Gaps 9;
Qy 382 RQVFFGAGNYHLVD-ENFDPDLPDYWLSLLPKFLVGTGTVKVLMAVSGSKRRKRLRVYLHCTNT 440
Db 12 RQSLIG-GNYGLLNTTNTFNPDIYSALIRQLMGRKALFTTSGTK--KIRSYTHCA-- 66
Qy 441 DNPYKEGDLTIYAINLHNV-----TKYLRPLYPFNSKNQVDKYLRLPL 483
Db 67 ---RQSKG-ITVLLMLNDTNTTVVAKVELNNSFSRLRHKMK-----SYKRASSQLFG-- 115
Qy 484 GPHGLL-----SKSVQLNGLTLKMWDDQTLPLMEKPLRPGSSIGLPAFS 528
Db 116 GPNGVIQREYHLYTAKGNLHSGTMLLGNALQVNSMGDLPPPIEPIHINSTEPIIAPYS 175
Qy 529 YSFFVIIRNAKVAAC 542
Db 176 IVFVHMENVVPAC 189
RESULT 4
T49648
hypothetical protein B8B20.20 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25022
A:Accession: T49648
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2298 <SCH>
A:Cross-references: UNIPROT:Q96U00; UNIPARC:UPI000017B4BA; EMBL:AL355933; GSPDB:GN00116;
A:Experimental source: BAC clone B8B20; strain OR74A
C:Genetics:
A:Gene: NCSP:B8B20.20
A:Map position: 6
A:Introns: 426/3
Query Match 3.9%; Score 112; DB 2; Length 2298;
Best Local Similarity 19.3%; Pred. No. 19;
Matches 114; Conservative 79; Mismatches 190; Indels 208; Gaps 28;
Qy 78 PKLTLTARGLSPA-----YLRFGGTKTDFLIFDPKKESTFEERSYQSQV-NQDIC 127
Db 1447 PRVDLIERLITPSNAHKEACLINIRAWQLARLVVNSGEGSASPRPFTTWRNNVFNQILD 1506

Qy 128 KYGSIPTDVEBKL-LEWPYQEQLLREHYQKFKKSTYSRSSVDVLYTFAN 178
Db 1507 QYMSAESDIEQQFRALSANMRSIDAAREELITKN-----KATALDILHTSAR 1555
Qy 179 CSGLDLIFGLNAL-----LRTADLQ-----WNSSNAQLLLDYCSSKGYNI 218
Db 1556 AS-LDVILKQAKLEAAIYTLNVTLQKMCYTLHFGSPGPDGILNVAL-----DTHAHFL 1609
Qy 219 SW-ELGNEPNSFLKADIFINGSQGBDFIQLHKLLRKSTPKNAKLYGPDVGOPRRRTAK 277
Db 1610 GWIETSSEQYSSNESSADIPRQLEDAILLQEKLTKEFPWA-----RELLAL 1659
Qy 278 MLKSLFKAGGEVID-SVTHHHYLYNGRTATREDPLNFDVLDIFISSVQKVFQVVESTPRG 336
Db 1660 PLKAITTFGQTEQVACTEKTVTTLAAKLAAR-----FIQ--ERVTVQLVFPQPG 1706
Qy 337 K-----KVMIGETSSAYGGGAPLLSDTFAAG-----FWLDK 368
Db 1707 KYGLFDPMPKMSGPERWL-----PLFIATLVNKNVDFDKDIETNILLSLVQS 1755
Qy 369 LGLSAR-MGIEVVMRQVFFGAGNYHL--VDENFDPLDYLWLSL-LFKKLVG--TKVL--- 419
Db 1756 IIKPMRFLGYETYLEAVLQGRGLPFLAEADVSAAGMTDYNHLDLFSRAIHYMRKALRG 1815
Qy 420 -----MASVQSGK-----RRKLRYVYLHCTNTDNPRYKEGDLTYLAINLHNVTXYL 464
Db 1816 ATTPAPGVTSSASTAGSSAQSIIRROREFSH-----1847
Qy 465 RLPPYPSNKKQVYLLPLG-----PHGLLSKSVQLNGLTLKMWYD-- 504
Db 1848 TLQAMTNIRKDLFLRLSLALADPTASTTEHRDYMAFTGLIS-LIKSHGVGIVVVDSE 1906
Qy 505 -----DOTLPLMEKPLRPG-----SSLGLPAPSYSF-FVIRNAKVA 540
Db 1907 FLTPSDSYSPLOPQLHTAGIMAYGVLSEKDVPAASQLFWLYFNNEKVA 1957
RESULT 5
T10666
hypothetical protein F6E21.40 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10666
R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancroft
submitted to the Protein Sequence Database, June 1999
A;Reference number: 216533
A;Accession: T10666
A;Molecule type: DNA
A;Residues: 1-670 <BB>
A;Cross-references: UNIPROT:Q9M090; UNIPARC:UPI000000A4F11; EMBL:AL049914; GSPDB:GN00062;
A;Experimental source: cultivar Columbia; BAC clone F6E21
C;Genetics:
A;Gene: ATSP:F6E21.40
A;Map position: 4
A;Introns: 47/3; 87/1; 123/3; 203/3; 230/2; 255/3; 284/3; 305/1; 335/3; 347/3; 370/3; 39
C;Superfamily: Schizosaccharomyces pombe negative regulator of mitosis skbl
Query Match 3.9%; Score 111; DB 2; Length 670;
Best Local Similarity 22.4%; Pred. No. 3.5;
Matches 123; Conservative 77; Mismatches 194; Indels 156; Gaps 33;
Qy 51 LVSPSFLSVTIDANLATDPRFLIILGSPKRLTLARGLSPAY--LRFGGTKTDFLIPOPK- 107
Db 47 LVDESYPSPVLEGN-GVDTQVLPVCGSDLV-----LSPQSWSHVVGVKISSWIDLSDSE 99
Qy 108 -----KESTPEERSYQSQVNODICKYGISPPDVEBKLREWPYQBLRLREHYQKFKF 161
Db 100 EVLRMDSETTLKQBIAMATHLSLQMB-----PD-----LTRPHYLAGGL 139
Qy 162 NSTYSRSV---DVLY-----TFANCS--GLDLIFGLNALLRTADLQWNSNAQLL 207
Db 140 RVSCCRSSFISDETFLYKITFNQALTFCGSLFLCNVISALKMLRVLPLVK---SEGDSM 196

Qy 208 LDYCSSKGYNISWELGN-----EPNSFLKA-DIFIN-----GSQLEDFTQLHKLL 253
Db 197 DD--TSGLNDSWELMNSFRLLCHEHDSKLSVALDVLSTLPSETSLGRWMGES-VRAAII 253
Qy 254 RKSTFKNAKLYGPDVGOP--RRKTAKMLKSLF-KAGEVIDSVTHHHYLYNGRTATREDF 310
Db 254 TDAFLTNAR-----GYPCLSKRHKQLTAGFFDHAQAVVICGKPVHNLKPLDSSSSGTE 307
Qy 311 LNPDLVDLIFISSVQKVFQVVESTPRGKRWLGETSSAYGGGAPLLSDTFAAGFMWLDKLG 370
Db 308 KNP--LRIYLDYVAYLFQKVESLSEQUIELGYRDFLQAPLQPLMDNLEAQTETFE--- 362
Qy 371 LSARMGLEVMRQVFFGAGNYHLVDENFDPLDYLWLSLFLFKKLVTGTYKLM- 420
Db 363 ---RDSVKYIYQ---RAVEKALVDR---VPDEKASEL-----TTVLVVGAGRGPLV 406
Qy 421 -ASVQSGKR--RKLRYVYLHCTNTDNPRYKEGDLTYLAINLHNVTK-----YLRUPY 468
Db 407 RASLQAAETDRKLKVT---AVEKNFN-----AVTTLHNLVQMEGWEDVVTIISCDM 455
Qy 469 PFSN--KQVDKYLLRPLGPHGLLSKSVQLNGLTLKMWDDQTLPLM---EKPLRPGSSLG 523
Db 456 RFWNAPEQADILVSELLGSFG-----DNELSPEDLDGAQRFKLP-DGIS 498
Qy 524 LPAPSYSFV 533
Db 499 IPS-SYTSFI 507
RESULT 6
S32961
hypothetical protein YBR259w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR1727
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S32961; S46140
R;Doignon, F.; Biteau, N.; Crouzet, M.; Aigle, M.
Yeast 9, 189-199, 1993
A;Title: The complete sequence of a 19,482 bp segment located on the right arm of chrom
A;Reference number: S29348; MUID:93220397; PMID:8465606
A;Accession: S32961
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-688 <DOI>
A;Cross-references: UNIPROT:P38338; UNIPARC:UPI000013A298; EMBL:X70529; NID:g1907246; P
R;Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45940
A;Accession: S46140
A;Molecule type: DNA
A;Residues: 1-688 <AIG>
A;Cross-references: UNIPARC:UPI000013A298; EMBL:Z36128; NID:g536684; PIDN:CAA85222.1; P
C;Genetics:
A;Cross-references: SGD:S0000463
A;Map position: 2R
C;Superfamily: Saccharomyces cerevisiae hypothetical protein YBR259w
Query Match 3.9%; Score 111; DB 2; Length 688;
Best Local Similarity 22.5%; Pred. No. 3.6;
Matches 67; Conservative 45; Mismatches 94; Indels 92; Gaps 16;
Qy 126 ICKYISPPDVEBKLREWPYQBLRLREHYQKFKKSTYSRSS-----VDVLYT 175
Db 164 MAEYSSKWKSDDRQLQOFMYEPRMKLKECLVFYENFDLQKSDPLKELIIPWEKIVYV 223
Qy 176 FANCSGLDLIFGLNALLRTADLQWNSN-----AQLLD-----YCSKGY- 216
Db 224 -ANC--IDAFTGQVRIDGAELIWTSKNLVFSISSAVLRNLNDLQNMFSAPRPYGEALV 280
Qy 217 -----NLSWELGNFENSLKKA---DIF--INGSQLG--EDFIQLHKLLRK- 255
Db 281 QDFAHIRSLKWSNDKVESLIRALIFNDMPFYFNKEQVDTKADGIFFLRLLRKFKHEIN 340

Qy 256 -----STFKN--AKLYGPDVGOPRRKTKAMLSFLKAGGEV-----IDSV 293
Db 341 DVKDFHIQVIKVLNSQFNKYSTLTMTSSKTQDRKSHNMPSSILDDGNKIGHVSPIDE- 399
Qy 294 TWHYYLNG-----RTATREDFLNPDLVDFISSVQKVQFVVESTR---PGKK 338
Db 400 -YSHFDNDPLWRDKVPKYVTNEQTPTDASAIKFD--HKVIAISLLRAYLPEKR 454

RESULT 7
F64383
hypothetical protein MJ0670 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: F64383
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Ison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: F64383
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-356 <BUL>
A:Cross-references: UNIPROT:Q58084; UNIPARC:UPI0000139BAF; GB:U67514; GB:L77117; NID:g28
C:Genetics:
A:Map position: REV596956-595886
A:Start codon: GTG

Query Match 3.9%; Score 110.5; DB 2; Length 356;
Best Local Similarity 21.0%; Pred. No. 1.4;
Matches 82; Conservative 49; Mismatches 155; Indels 105; Gaps 15;

Qy 126 ICKY-----GSTPPDVEKRLLEWYQQLLREHYQKKFNKSTYSRSVD----- 171
Db 14 IRKYMKIYGNKEKDIERLIKE-----LKEEHLVETEDGYTLKAEDEEEMHSHKV 66
Qy 172 -----VLYTFANCGLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNPE 226
Db 67 GALKAEAIYKFAKPS-----KITDL-----SNPR-VLDLCSGMGYNIAALHYNK 109
Qy 227 NSFLKKADIF-----INSGLEDIFQLHLKLRKTKFNKALYGPDV 268
Db 110 NAEIDMVFICEVFLFLFLDIPYKEHIIKDKREYFNKIGIEYKSDYNINLY---V 166
Qy 269 GOPRRKTKMLKSLFKAGGEVIDSVTHHYLYNGRTAT--REDFLNPDLVDFISSVQKV 326
Db 167 GDARFIIKSDKY-----NVVFDATSPKEDPTLYTYDFL-----KEI 205
Qy 327 FQVVESTRPGKKWMLGETSSAYGGAPLLSDPTFAAGFMWLDKGLSARMGIEVVMRQVFF 386
Db 206 YKRMEDN--GVLI-----SYSSAIPFRSALVDCGFVISEKESVGRKRGTILAYKNPF 256
Qy 387 GAGNVHLVDENPD-----PLPDYWSLLPKLVGTVKVLMAVSGSRKRLRVLHCTN 439
Db 257 KPNRINEVDERVIALSVIALPYRDETSLTKDIEDREERREKLKELKIGKYLSTQK 316
Qy 440 TDNPRYKGGDLYA--INLHNVTYKRLPY 468
Db 317 IYKGNIPPEILKIQKEDLNSSEIIKKMLKPF 347

RESULT 8
Tl2094
beta-fructofuranosidase (EC 3.2.1.26) - fava bean
C:Species: Vicia faba (fava bean)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: Tl2094
R:Weber, H.; Borisjuk, L.; Heim, U.; Buchner, P.; Wobus, U.
Plant Cell 7, 1835-1846, 1995
A:Title: Seed coat-associated invertases of fava bean control both unloading and storage

A:Reference number: Z17416; MUID:96093423; PMID:8535137
A:Accession: Tl2094
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-575 <WEB>
A:Cross-references: UNIPROT:Q43855; UNIPARC:UPI000009D74A; EMBL:Z35162; NID:g861154; PID:1
A:Experimental source: cv. Fribo, seed coat
C:Genetics:
A:Gene: CWINV1
C:Superfamily: beta-fructofuranosidase
C:Keywords: cell wall; glycoprotein; glycosidase; hydrolase

Query Match 3.8%; Score 107.5; DB 2; Length 575;
Best Local Similarity 21.1%; Pred. No. 5;
Matches 71; Conservative 49; Mismatches 107; Indels 109; Gaps 19;

Qy 46 QSPHLVLS-----PSFLSVTIDANLATDPRFLILGSPKRLTLARGLS-----P 89
Db 228 KPHIHSAKRTGMWECPPDFYPVSLGKGNLD--LSMMGMNVKHLKNSLDITRYEYYTIG 285
Qy 90 AYLR-----FGTKTDF-----LIFDPKKESTFEERSYW-----QSQVNO 124
Db 286 TYLQNDQKYPDKTSEDCWGLRYDGNFYASKSFDFPTK-----NRRRIIWMANESDTKE 341
Qy 125 DICKYG-----SIPPDV-----BEKRLLEWYQQLLLR-----EHYQKKFNKSTYSRSV 170
Db 342 DDVKKGWAGTQAIPTTWLDSRRQLR-QMPVEHLNRLRGQVEMKRLKKGCGY-----L 396
Qy 171 DVLYTFANCGLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNPEPSFL 230
Db 397 EVKGITASQADVEVTFSSFLDKAEAFDPNWEAE---DLCAQKSGKVRGGVG--PFGLL 451
Qy 231 KKADIFNGSLQGEDFIQL-----HKLL-----RKSTFFKNALYGP-----DV 268
Db 452 TLA-----SKLEEYTSVFRVFAANKHKILCMCSDAKSSSLNRELYKPSFAGFVNVDL 505
Qy 269 GOPRRKTKMLKSLFKAGGEVIDSVTHHYLYNGRT 304
Db 506 GNNKLSLRSL-----IDHSVVESFGVGKT 531

RESULT 9
T38446
microtubule-associated protein ssm4 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38446; T00012
R:McDougall, R.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, December 1997
A:Reference number: Z21793
A:Accession: T38446
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-670 <MCD>
A:Cross-references: UNIPROT:O42667; UNIPARC:UPI0000135FDD; EMBL:AL009227; PIDN:CAA15832.
A:Experimental source: strain 972h-; cosmid c27D7
R:Yamashita, A.; Watanabe, Y.; Yamamoto, M.
Genes to Cells 2, 155-166, 1997
A:Title: Microtubule-associated coiled-coil protein Ssm4 is involved in the meiotic deve
A:Reference number: Z14042; MUID:97311255; PMID:9167972
A:Accession: T00012
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-670 <YAM>
A:Cross-references: UNIPARC:UPI0000135FDD; EMBL:AB000269; NID:g3341860; PIDN:BAA31857.1.1;
C:Genetics:
A:Gene: ssm4; SPAC27D7.13c
A:Map position: 1

Query Match 3.7%; Score 106; DB 2; Length 670;
Best Local Similarity 21.4%; Pred. No. 8.2;
Matches 80; Conservative 58; Mismatches 149; Indels 86; Gaps 15;

RESULT 12
S00652
A:Title: phosphoribosylamine-glycine ligase (EC 6.3.4.13) - fission yeast (*Schizosaccharomyces pombe*)
N:Alternate names: AifSase; aminimidazole ribotide synthetase; CARSase; glycylamide rib
N:Contains: phosphoribosylamine-glycine ligase (EC 6.3.4.13); phosphoribosylformylglycin
C:Species: *Schizosaccharomyces pombe*
C:Date: 07-Sep-1990 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C:Accession: S00652; T40496; T40422
R:McKenzie, R.; Schuchert, P.; Kilbey, B.
Curr. Genet. 12, 591-597, 1987
A:Title: Sequence of the bifunctional adel gene in the purine biosynthetic pathway of th
A:Reference number: S00652; MUID:89003164; PMID:3502942
A:Accession: S00652
A:Molecule type: DNA
A:Residues: 1-788 <MCK>
A:Cross-references: UNIPROT:P20772; UNIPARC:UPI0000132A3F; EMBL:X06601; NID:G4903; PIDN:
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duisterhoeft, A.
submitted to the EMBL Data Library, February 1998
A:Reference number: Z21910
A:Accession: T40496
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-788 <WOO>
A:Cross-references: UNIPARC:UPI0000132A3F; EMBL:AL021730; PIDN:CAA16823.1; GSPDB:GN00067
A:Experimental source: strain 972h-; cosmid c4C3
R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, March 1999
A:Reference number: Z21928
A:Accession: T40422
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 604-788 <SEE>
A:Cross-references: UNIPARC:UPI000016908D; EMBL:AL035655; PIDN:CAB38600.1; GSPDB:GN00067
A:Experimental source: strain 972h-; cosmid c405
C:Genetics:
A:Gene: ADE1; SPDB:SPBC405.01
A:Map position: 2
C:Superfamily: Saccharomyces cerevisiae ADE5 multifunctional protein; phosphoribosylamin
C:Keywords: cyclo-ligase; purine nucleotide biosynthesis
F:5-425/Domain: phosphoribosylamine-glycine ligase homology <PGL>
F:438-767/Domain: phosphoribosylformylglycinamide cyclo-ligase homology <PFCL>

Query Match 3.7%; Score 104.5; DB 1; Length 788;
Best Local Similarity 27.7%; Pred. No. 13;
Matches 70; Conservative 36; Mismatches 114; Indels 33; Gaps 11;
QY 297 HYILNGRTATRE--DFLNPDV-LDIFISSVQKVQFVVEST-RPGKKVWLGETSSAY---- 348
DB 424 HHALNPKRTRREILTYENSGVSDVNGNEFVQRIKDLVKSTRPRGADADIGGFGGIFDLKQ 483
QY 349 -GGGAPLL-SDTFAAGFWMLDKGLSAR--MGIEVVMQVFPFGAGNYHLVDENFDPL--P 402
DB 484 AGWNPDLVSATDGVGSKLLALSINKHDTVGIDLVANV-----NDLVVQGAEPFLFL 537
QY 403 DYWLSSLPFKLVGTVKVLMAVQSGSKRKLRYVLHCTNTDNPYKSGDITLYAINLHNVTK 462
DB 538 DYFATGSLDLKVSTSFVEGVGKQKQACALVGGTSEMPGLYHDGHYDANGTSVGAVS 597
QY 463 YRLPYPPSNKQVDKYLRLPLGPHGLLSKSVQLNGTL--KWDV-----DOTLPLMEKPL 516
DB 598 DDILPKPESFSGKDILL-----GLASDGVHNSGYSLVKRKIVEYSDLEYTSVCPWDKNV 650
QY 517 RPSGLGLPAF5Y 529
DB 651 RLGDSLLIPTRII 663

RESULT 13
F70411
adenylosuccinate synthetase - Aquifex aeolicus
C:Species: Aquifex aeolicus

C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: F70411
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: F70411
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-432 <AOQ>
A:Cross-references: UNIPROT:O67321; UNIPARC:UPI00000565A2; GB:AE000733; NID:G2983720; PI
A:Experimental source: strain VF5
C:Genetics:
A:Gene: purA
C:Superfamily: adenylosuccinate synthase

Query Match 3.7%; Score 104; DB 2; Length 432;
Best Local Similarity 23.9%; Pred. No. 5.9;
Matches 96; Conservative 39; Mismatches 128; Indels 138; Gaps 22;
QY 15 LLLGLPLGSPGALPRPAQADVVLDL-----FFTOEPLHLVSPS 55
DB 51 ILHLLPTGILHEHVKGVIQGM-VVDLEVLHKEVNLEEKGIYVKERLIFISDRAHLVMPY 109
QY 56 FLSTVIDANLATDPRFLLILGSPK--LRTLARGLSPAYL-RFGGKTDFLIFDPKKESTF 112
DB 110 H-----KLLDSLFKKKGITGLRGIPAYMFYK--RKGIKIRISDLKDEKRF 154
QY 113 EERSYQSQVNQDICKYSIPDPVEEK-----LRLEWPHYQEQLLREHYQKKFQNSTY 165
DB 155 ----YTLLEDNLDVFK-----NICEKVFCEKFDLDINQIYEQL----RYFEFKEVNV- 199
QY 166 SRSVDVLYTFPANGSGLDLIFGLNALLRTADL-----QWNSNAQLLDLYCCKSGKGVNISWE 221
DB 200 ---VDLLRPNTQKGSVLPBGAQGTLLDVMGTYPVYVTSNASAL-----GLSNG 246
QY 222 LGNEPNSFLKADIFING-----SQL-GEDFIQLHKLRLKSTFFKNAKLYG 265
DB 247 TGMPPKYF---SDAFFLGVAKAYTRVGEPPFTLKGEGEKEKREL-----GGBYG 295
QY 266 PDVGPQRR---KTAKMLKSLFKAGGEVIDSVTHHHYINGRTATREDPLNP----- 313
DB 296 STTGPRRCGWLDLVALKYAVQVNG-----LDGFVITKLDVLDTFDEVKVCVA 343
QY 314 ----DVLIDIFISSVQKVQFV--VESTRPKKVWLGETSSA 347
DB 344 YELDGEVIDYPPASVSELIRVKPVVKTLKG---WKKSTKGA 381

RESULT 14
D97065
transketolase [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
A:Accession: D97065
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: D97065
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-796 <KUR>
A:Cross-references: UNIPROT:Q97JE3; UNIPARC:UPI0000131969; GB:AE001437; PIDN:AAK79311.1,
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1343
C:Superfamily: phosphotetolase

Query Match 3.7%; Score 104; DB 2; Length 796;
Best Local Similarity 21.6%; Pred. No. 15;

Query Match	3.7%; Score 104; DB 2; Length 2013;
Best Local Similarity	20.6%; Pred. No. 60;
Matches	95; Conservative 64; Mismatches 161; Indels 142; Gaps 21;
Qy	5 SKPALPPLMLLLGLPLSPGALPPAQAQVDVLD-----FFT 45 : : : : :
Db	256 AKGPVPMNLKATL---SGENSAGATYPAEKTTTVNLEENSSNLDYPITAGDNWAFSM 312 : : : : :
Qy	46 QEPHLVSPFLSV--TIDANLATDPRELILLGSPKLRTIARG-----LSPAYLR 93 : : : : :
Db	313 KELAFSLKPGGYTIOWPEIOKKSENKFNKL-----KLEFLKNGGDIIISVNTADPVVIR 368 : : : : :
Qy	94 FG-----GTKTDFLI FDPKESTFBEERSYQSQVNQDICKYGSI PPDVEEKLRL 143 : : : : :
Db	369 FGEPPYSQLSTVNCKANVLNDEKQ-----VVVEYGFIVANIYQRTQVS 412 : : : : :
Qy	144 WP-----YEQALLRHHYQKKFNKNSTRSSVDLVTFANCSDL 184 : : : : :
Db	413 MAAKIPADAVKGTEYTGTVNVYDEDLIVTSIKITEVTDSATSIADVSKVSKTSISEGDV 472 : : : : :
Qy	185 IFGLNALLRTADIOWN-----SSNA-----QLLLDYCSSKGNYI-SWEELGNEPSFLKKAD 234 : : : : :
Db	473 -----LEWGMFPRISSAAPGVNDIEIVAPIPKGITKVLSYTPNNNSMASMKKLE 520 : : : : :

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 27, 2006, 17:43:52 ; Search time 234 Seconds
(without alignments)
1637.187 Million cell updates/sec

Title: SEQ2-246PHE
Perfect score: 2841
Sequence: 1 MLRSKPALPPPLMLLLGSP.....LPAFSYFFVIRNAKVAACI 543

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_05-80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2841	100.0	543	2	Q9Y251_HUMAN
2	2834	99.8	543	2	Q53GE5_HUMAN
3	2820	99.3	545	2	Q9UL39_HUMAN
4	2285	80.4	545	2	Q9MYX0_BOVIN
5	2153	75.8	535	2	Q8K3K3_MOUSE
6	2143	75.4	535	2	Q6YGI1_MOUSE
7	2138	75.3	536	2	Q71RPI_RAT
8	2126	74.8	536	2	Q9QZF8_RAT
9	1648.5	58.0	523	2	Q90VK5_CHICK
10	1320	46.5	533	2	Q4SYF6_TETNG
11	1150.5	40.5	592	2	Q9HB37_HUMAN
12	1147.5	40.4	592	2	Q5VUH6_HUMAN
13	1142.5	40.2	592	2	Q8WQK2_HUMAN
14	1036.5	36.5	597	2	Q4TB80_TETNG
15	1017.5	35.8	548	2	Q5VUH4_HUMAN
16	1011.5	35.6	548	2	Q8WQK1_HUMAN
17	932.5	32.8	534	2	Q9HB38_HUMAN
18	929.5	32.7	534	2	Q5VUH5_HUMAN
19	893.5	31.5	480	2	Q9HB39_HUMAN
20	742.5	26.1	255	2	Q4TGC8_TETNG
21	699	24.6	515	2	Q8T108_BOMMO
22	417	14.7	521	2	Q9SDA1_ARATH
23	417	14.7	543	2	Q9F10_ARATH
24	400	14.1	559	2	Q89F99_BRAJA
25	388	13.7	526	2	Q5SNA6_ORYSA
26	379	13.3	541	2	Q69116_ORYSA
27	377	13.3	527	2	Q9LRC8_SCURA
28	365	12.8	537	2	Q70YJ3_HORVU
29	363	12.8	536	2	Q9FZP1_ARATH
30	353.5	12.4	516	2	Q9FLK8_ARATH
31	353.5	12.4	539	2	Q8L608_ARATH

32	350.5	12.3	529	2	Q6ZJ22_ORYSA	Q6zje2 oryza sativ
33	169.5	6.0	190	2	Q82604_ARATH	Q82604 arabidopsis
34	156	5.5	935	2	Q9VE79_DROME	Q9ve79 drosophila
35	141	5.0	559	2	Q7SEB0_NEUCR	Q7seb0 neurospora
36	138.5	4.9	463	2	Q63T97_BURPS	Q63t97 burkholderi
37	138	4.9	1128	2	Q5IT65_ANOGA	Q5tte5 anopheles g
38	126.5	4.5	493	2	Q9HK01_THEAC	Q9hk01 thermoplasm
39	125.5	4.4	665	2	Q5SIC3_CRYNE	Q5sic3 cryptococcu
40	125.5	4.4	665	2	Q5K7V9_CRYNE	Q5k7v9 cryptococcu
41	124	4.4	634	2	Q5NJL7_9BACT	Q5njl7 uncultured
42	124	4.4	765	2	Q4P0C9_USTMA	Q4p0c9 ustilago ma
43	121	4.3	594	2	Q512T2_MAGGR	Q512t2 magnaporthe
44	119	4.2	511	2	Q55MH5_CRYNE	Q55mh5 cryptococcu
45	119	4.2	511	2	Q5K897_CRYNE	Q5k897 cryptococcu

ALIGNMENTS

RESULT 1

Q9Y251_HUMAN

ID Q9Y251_HUMAN PRELIMINARY; PRT; 543 AA.

AC Q9Y251;

DT 01-NOV-1999 (Tremblrel. 12, Created)

DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)

DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)

DE Heparanase.

GN Name=HPA; Synonyms=HPSE;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Placenta;

RX MEDLINE=99321249; PubMed=10395326; DOI=10.1038/10525;

RA Hulett M.D., Freeman C., Hamdorf B.J., Baker R.T., Harris M.J., Parish C.R.;

RA "Cloning of mammalian heparanase, an important enzyme in tumor invasion and metastasis.";

RT Nat. Med. 5:803-809(1999).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RA Vlodavsky I., Friedman Y., Elkin M., Aingorn H., Atzmon R., Ishai-Michaeli R., Bitan M., Pappo O., Peretz T., Michal I., Spector D., Pecker I.;

RA "Mammalian heparanase: a novel gene involved in tumor progression and metastasis.";

RT Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Placenta;

RX MEDLINE=99335379; PubMed=10405343; DOI=10.1006/bbrc.1999.0962;

RA Kussie P.H., Hulmes J.D., Ludwig D.L., Patel S., Navarro E.C., Seddon A.P., Giorgio N.A., Bohlen P.;

RA "Cloning and functional expression of a human heparanase gene.";

RT Biochem. Biophys. Res. Commun. 261:183-187(1999).

RN [4]

RP NUCLEOTIDE SEQUENCE.

RC MEDLINE=99377052; PubMed=10446189; DOI=10.1074/jbc.274.34.24153;

RA Toyoshima M., Nakajima M.;

RA "Human heparanase. Purification, characterization, cloning, and expression.";

RT J. Biol. Chem. 274:24153-24160(1999).

RN [5]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Pancreas;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zengerg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Bufterfield Y.S.N., Krzywinski M.I., Skalska U., Scallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.:
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[6]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pancreas;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
[7]
RP NUCLEOTIDE SEQUENCE.
RA Pinhal M.A., Semedo P.;
RT "Cloned heparanase from MCF-7 cells.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF144325; AAD41342.1; -; mRNA.
DR EMBL; AF152376; AAD45669.1; -; mRNA.
DR EMBL; AF155510; AAD54941.1; -; mRNA.
DR EMBL; AF165154; AAD45379.1; -; mRNA.
DR EMBL; AY948074; AAX47106.1; -; mRNA.
DR EMBL; BC051321; AAH51321.1; -; mRNA.
DR EMBL; ENSG00000173083; Homo sapiens.
DR GO; GO:0004566; F:beta-glucuronidase activity; TAS.
DR GO; GO:0006029; P:proteoglycan metabolism; TAS.
DR InterPro; IPR005199; Glyco hydro 79_N.
DR Pfam; PF03662; Glyco_hydro_79n; I.
FT CHAIN 158 543 heparanase.
SQ SEQUENCE 543 AA; 61118 MW; AD262EC267FC4AB2 CRC64;

Query Match 100.0%; Score 2841; DB 2; Length 543;
Best Local Similarity 100.0%; Pred. No. 3.5e-205;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLRSKPALPPPLMLLLGPGPLSPGALPRPAQAQDVVDLDFFTQEPHLVSPSFLSVT 60
Db 1 MLLRSKPALPPPLMLLLGPGPLSPGALPRPAQAQDVVDLDFFTQEPHLVSPSFLSVT 60

Qy 61 IDANLATDPRFLILGSPKRLTLARGLSPAYLRFGGTKTDFLIIDPKKESTFEERSYQWS 120
Db 61 IDANLATDPRFLILGSPKRLTLARGLSPAYLRFGGTKTDFLIIDPKKESTFEERSYQWS 120

Qy 121 QVNQDICKYGSIPDPVEEKLREWPYQQLLLREHYQKKFNKSTYSRSSVDVLYTFNACS 180
Db 121 QVNQDICKYGSIPDPVEEKLREWPYQQLLLREHYQKKFNKSTYSRSSVDVLYTFNACS 180

Qy 181 GLDLIFGLNALLRTADLQWNSNAQALLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Db 181 GLDLIFGLNALLRTADLQWNSNAQALLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240

Qy 241 QLGEDFIQLHKLRLKSTFNKAKLYGPDVGQPPRRKTKAKMLKSLFKAGGEVIDSVTWHHYL 300
Db 241 QLGEDFIQLHKLRLKSTFNKAKLYGPDVGQPPRRKTKAKMLKSLFKAGGEVIDSVTWHHYL 300

Qy 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTREGKVKWLGETSSAYGGGAPLLSDTFA 360
Db 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTREGKVKWLGETSSAYGGGAPLLSDTFA 360

Qy 361 AGFMWLDKLGLSARMGIEVWVRQVFFGAGNTHLVDFNDPLPDYWLSLFLFKLVGTQKVL 420
Db 361 AGFMWLDKLGLSARMGIEVWVRQVFFGAGNTHLVDFNDPLPDYWLSLFLFKLVGTQKVL 420

Qy 421 ASVQGSKRRKLRLVYLHCTNTDNPVYKEGDLTLVAINLHNVTKYLRLPYPFNSNKQVDKYL 480

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Db 421 ASVQGSKRRKLRLVYLHCTNTDNPVYKEGDLTLVAINLHNVTKYLRLPYPFNSNKQVDKYL 480
Qy 481 RPLQPHGLLSKSVQLNGLTLLKVVDDQTLPLPMLKPLRPGSLGLPAFYSFFVIRNAKVA 540
Db 481 RPLQPHGLLSKSVQLNGLTLLKVVDDQTLPLPMLKPLRPGSLGLPAFYSFFVIRNAKVA 540
Qy 541 ACI 543
Db 541 ACI 543

RESULT 2
Q53GE5_HUMAN PRELIMINARY; PRT; 543 AA.
AC Q53GE5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Heparanase variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human small intestine;
RA Maruyama K., Sugano S.;
RT "Oligo-capping : a simple method to replace the cap structure of
RT eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174 (1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human small intestine;
RA Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
RT end-enriched cDNA library.";
RL Gene 200:149-156 (1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human small intestine;
RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK222986; BAD96706.1; -; mRNA.
FT NON_TER 1
SQ SEQUENCE 543 AA; 61118 MW; AC392EC267FC4AB2 CRC64;

Query Match 99.8%; Score 2834; DB 2; Length 543;
Best Local Similarity 99.8%; Pred. No. 1.2e-204;
Matches 542; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLRSKPALPPPLMLLLGPGPLSPGALPRPAQAQDVVDLDFFTQEPHLVSPSFLSVT 60
Db 1 MLLRSKPALPPPLMLLLGPGPLSPGALPRPAQAQDVVDLDFFTQEPHLVSPSFLSVT 60

Qy 61 IDANLATDPRFLILGSPKRLTLARGLSPAYLRFGGTKTDFLIIDPKKESTFEERSYQWS 120
Db 61 IDANLATDPRFLILGSPKRLTLARGLSPAYLRFGGTKTDFLIIDPKKESTFEERSYQWS 120

Qy 121 QVNQDICKYGSIPDPVEEKLREWPYQQLLLREHYQKKFNKSTYSRSSVDVLYTFNACS 180
Db 121 QVNQDICKYGSIPDPVEEKLREWPYQQLLLREHYQKKFNKSTYSRSSVDVLYTFNACS 180

Qy 181 GLDLIFGLNALLRTADLQWNSNAQALLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Db 181 GLDLIFGLNALLRTADLQWNSNAQALLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240

Qy 241 QLGEDFIQLHKLRLKSTFNKAKLYGPDVGQPPRRKTKAKMLKSLFKAGGEVIDSVTWHHYL 300
Db 241 QLGEDFIQLHKLRLKSTFNKAKLYGPDVGQPPRRKTKAKMLKSLFKAGGEVIDSVTWHHYL 300

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QY 301 NGRATATREDFLNPVDLIDIFISSVQKVFQVVESTTRPGKVKWLGETSSAYGGGAPLLSDTFA 360
DB 301 NGRATATREDFLNPVDLIDIFISSVQKVFQVVESTTRPGKVKWLGETSSAYGGGAPLLSDTFA 360
QY 361 AGFWMLDKLGLSARMGIEVVMRQVFFGAGNHYHLDENFDPLPDYWLKLLFKKLVGTGVLM 420
DB 361 AGFWMLDKLGLSARMGIEVVMRQVFFGAGNHYHLDENFDPLPDYWLKLLFKKLVGTGVLM 420
QY 421 ASVQSGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTYKLRLLPYFSPSNKQVDKYL 480
DB 421 ASVQSGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTYKLRLLPYFSPSNKQVDKYL 480
QY 481 RPLGPHGLLSKSVQLNGITLKWVDDQTLPLPMEKPLRPGSSGLGPAFYSFFVIRNAKVA 540
DB 481 RPLGPHGLLSKSVQLNGITLKWVDDQTLPLPMEKPLRPGSSGLGPAFYSFFVIRNAKVA 540
QY 541 ACI 543
DB 541 ACI 543

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RESULT 3

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Q9UL39_HUMAN
ID Q9UL39_HUMAN PRELIMINARY; PRT; 545 AA.
AC Q9UL39;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Heparanase.
GN Name=HPSE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=20229546; PubMed=10764835; DOI=10.1093/glycob/10.5.467;
RA Dempsey L.A., Plummer T.B., Coombes S.L., Platt J.L.;
RT "Heparanase expression in invasive trophoblasts and acute vascular
RT damage."
RL Glycobiology 10:467-475 (2000).
DR EMBL; AF084467; AAD54516.1; -; mRNA.
DR Ensembl; ENSG00000173083; Homo sapiens.
DR HGNC; HGNC:5164; HPSE.
DR InterPro; IPR005199; Glyco_hydro_79n.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 545 AA; 61417 MW; 67B80ACD73C5A9A1 CRC64;

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Query Match 99.3%; Score 2820; DB 2; Length 545;
Best Local Similarity 99.6%; Pred. No. 1.4e-203;
Matches 543; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 MLLRSKPPALPPP-LMLLLGLPLGSPGALPRPAQA-QDVVDLDFFTQEPHLVSPSFLS 58
DB 1 MLLRSKPPALPPP-LMLLLGLPLGSPGALPRPAQAQDVVDLDFFTQEPHLVSPSFLS 60
QY 59 VTDANLATDPRFLILGLSPKRLTLARGLSPAYLRFGGTKDTFLIFDPKKESTFEERSY 118
DB 61 VTDANLATDPRFLILGLSPKRLTLARGLSPAYLRFGGTKDTFLIFDPKKESTFEERSY 120
QY 119 OSQVQNDICKYGSIPDPVEEKLREWPYQQLLREHYQKKFNSTYSRSSVDVLYTFAN 178
DB 121 OSQVQNDICKYGSIPDPVEEKLREWPYQQLLREHYQKKFNSTYSRSSVDVLYTFAN 180
QY 179 CSGLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFIN 238
DB 181 CSGLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFIN 240
QY 239 GSQLGEDFIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHY 298
DB 241 GSQLGEDFIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHY 300

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QY 299 YLNGRTATREDFLNPVDLIDIFISSVQKVFQVVESTTRPGKVKWLGETSSAYGGGAPLLSDT 358
DB 301 YLNGRTATREDFLNPVDLIDIFISSVQKVFQVVESTTRPGKVKWLGETSSAYGGGAPLLSDT 360
QY 359 FAAGFWMLDKLGLSARMGIEVVMRQVFFGAGNHYHLDENFDPLPDYWLKLLFKKLVGTGV 418
DB 361 FAAGFWMLDKLGLSARMGIEVVMRQVFFGAGNHYHLDENFDPLPDYWLKLLFKKLVGTGV 420
QY 419 LMASVQSGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTYKLRLLPYFSPSNKQVDK 478
DB 421 LMASVQSGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTYKLRLLPYFSPSNKQVDK 480
QY 479 LLRLPGLPHGLLSKSVQLNGITLKWVDDQTLPLPMEKPLRPGSSGLGPAFYSFFVIRNAK 538
DB 481 LLRLPGLPHGLLSKSVQLNGITLKWVDDQTLPLPMEKPLRPGSSGLGPAFYSFFVIRNAK 540
QY 539 VAACI 543
DB 541 VAACI 545

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RESULT 4

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Q9MY10_BOVIN
ID Q9MY10_BOVIN PRELIMINARY; PRT; 545 AA.
AC Q9MY10;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Heparanase.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=21176669; PubMed=11277877;
RA Kizaki K., Nakano H., Nakano H., Takahashi T., Imai K., Hashizume K.;
RT "Expression of heparanase mRNA in bovine placenta during gestation."
RL Reproduction 121:573-580 (2001).
DR EMBL; AF281160; AAF87301.2; -; mRNA.
DR InterPro; IPR005199; Glyco_hydro_79n.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 545 AA; 61076 MW; FAC4BDFD855B933 CRC64;

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Query Match 80.4%; Score 2285; DB 2; Length 545;
Best Local Similarity 80.0%; Pred. No. 2.8e-163;
Matches 436; Conservative 34; Mismatches 73; Indels 2; Gaps 1;

QY 1 MLLRSKPPALPPP-LMLL--LLGLPLGSPGALPRPAQAQDVVDLDFFTQEPHLVSPSFLS 58
DB 1 MLLACRPGRLPPPLMLLLPLLLGLGSPGTPFAAAAADDAAELEFFTERPHLVSPAFLS 60
QY 59 VTDANLATDPRFLILGLSPKRLTLARGLSPAYLRFGGTKDTFLIFDPKKESTFEERSY 118
DB 61 FTIDANLATDPRFTFLGSSKRLTLARGLAPAYLRFGGNGKDFLIIDPKKEPAFEERSY 120
QY 119 OSQVQNDICKYGSIPDPVEEKLREWPYQQLLREHYQKKFNSTYSRSSVDVLYTFAN 178
DB 121 LSQSNQDICKSGSIPSDVEEKLREWPYQQLLREHYQKKFTNSTYSRSSVDMLYTFAS 180
QY 179 CSGLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFIN 238
DB 181 CSGLNIFGNALLRTDMHDSNAQLLDYCSSKGYNISWELGNEPNSFORKAGIFIN 240
QY 239 GSQLGEDFIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHY 298
DB 241 GROLGSDFIQKLLKLSAFKNAKLYGPDIGQPRNTVMKLSFLKAGGEVIDSVTWHY 300
QY 299 YLNGRTATREDFLNPVDLIDIFISSVQKVFQVVESTTRPGKVKWLGETSSAYGGGAPLLSDT 358
DB 301 YLNGRTATREDFLNPVDLIDIFISSVQKVFQVVESTTRPGKVKWLGETSSAYGGGAPLLSDT 360

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Db 301 YVNGRIATKDFLNPDIIDTFTISSVQKTLRIVEKIRPLKVKWLGETSSAFGGGAPFLSNT 360
Oy 359 FAAGFMWLDKGLSARMGIEVVMROVFCGAGNYHLVDNFPDPLDYWLSLFLPKLVGTFKV 418
Db 361 FAAGFMWLDKGLSARMGIEVVMROVFCGAGNYHLVDNFPDPLDYWLSLFLPKLVGNKV 420
Oy 419 LMASVQGSKRRLRVLYLHCTNTDNPRYKEGDLTLVAINLHNVTYKRLRYPFPFSNKQVDKY 478
Db 421 LMASVKGPDRSKFRVYLHCTNTKHPRYKEGDLTLVAINLHNVTYKRLRYPFPFSNKQVDKY 480
Oy 479 LLRLPGPHGLSKSVQLNGLTLKMVDQDTLPLPMEKPLRPSSGLPAPFSYFFVIRNAK 538
Db 481 LKPSGTDLGLSKSVQLNGQILKMVDEQTLPALTEKPLHPGSSLCMPFPFSYFFVIRNAK 540
Oy 539 VAACI 543
Db 541 VAACI 545

RESULT 5
QBK3K3 MOUSE
ID QBK3K3 MOUSE PRELIMINARY; PRT; 535 AA.
AC QBK3K3;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
DE Heparanase (Mus musculus 0 day neonate thymus cDNA, RIKEN full-length
DE enriched library, clone:A43010M04 product:heparanase, full insert
DE sequence).
GN Name=Hpsae; Synonyms=Hpa, Hape;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
[1]
RC STRAIN=FVB;
RA Miao H.-Q., Navarro E., Patel S., Sargent D., Koo H., Wan H.,
RA Plata A., Zhou Q., Ludwig D., Bohlen P., Kussie P.;
RT "Cloning, expression, and purification of mouse heparanase.";
RL Protein Expr. Purif. 0:0-0(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J.H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
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RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=1246851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yananaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Meglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[5]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[7]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Kato H., Kawai J., Kojima Y., Itoh M., Kagawa I., Kasukawa T.,
RA Horii F., Imotani K., Ishii Y., Konno S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takanashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[8]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwagi K.,
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RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[7]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
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RA Kato H., Kawai J., Kojima Y., Itoh M., Kagawa I., Kasukawa T.,
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RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takanashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
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RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
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RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[7]
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RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
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RA Tagawa A., Takanashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
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RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
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RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[7]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
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RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
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RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takanashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[8]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[7]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
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RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Kato H., Kawai J., Kojima Y., Itoh M., Kagawa I., Kasukawa T.,
RA Horii F., Imotani K., Ishii Y., Konno S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takanashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
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RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
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RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
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RL Genome Res. 10:1757-1771(2000).
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RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K
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RC STRAIN=SUJ/J; TISSUE=Spleen;
RA Hulet M.D., Wang J., Hornby J.R., Freeman C., Pagler E., McHenry J.,
RA Parish C.R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY077467; AAL76083.1; -; mRNA.
DR EMBL; AK040471; BAC30600.1; -; mRNA.
DR EMBL; AF395907; AAQ15188.1; -; mRNA.
DR Ensembl; ENSMUSG0000035273; Mus musculus.
DR MGI; MGI:1343124; Hspe.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); TAS.
DR InterPro; IPR005199; Glyco hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; I.
SQ SEQUENCE 535 AA; 60065 MW; 6E73A8302FBA0ADF CRC64;

Query Match 75.8%; Score 2153; DB 2; Length 535;
Best Local Similarity 76.8%; Pred. No. 2.4e-153;
Matches 408; Conservative 50; Mismatches 73; Indels 0; Gaps 0;
Qy 13 LMLLLGLPLSPGALPRPAQADVDLDFQTEPLHLVSPFLSVITDANLATDRPL 72
Db 5 LLLWLWGLGALAQAGAPAGTAPDDVVDLEFYTKRPLRSVSPFLSITIDASLATDRPL 64
Qy 73 ILLGSPKLRTLARGLSPAYLRFPGTKTDFELIFDPKKESTFEERSYQSQVNOQICKYGS 132
Db 65 TFLGSPRLRALARGLSPAYLRFPGTKTDFELIFDPKKESTFEERSYQSQVNOQICKYGS 124
Qy 133 PPDVEEKLRLWPYQEQALLREHYQKFKNSTYSSRSVDVLYTFPANCGLDLIFGLNALL 192
Db 125 SAAVLRKLVQEWPFQELLRLREYQKEFKNSTYSSRSVDVLYTFPANCGLDLIFGLNALL 184
Qy 193 RTADLQNSNAQALLDYCSSKGYNISWELGNPNFLKKADIPINGSQGLGEDFVLHKL 252
Db 185 RTPDLRWNSNAQALLDYCSSKGYNISWELGNPNFLKKADIPINGSQGLGEDFVLHKL 244
Qy 253 LRKSTFNKALYGPVQOPRRKTKAMLKSFKAGGEVIDSVTHHYLYNGRTATREDPLN 312
Db 245 LQSAFQNAKLYGPDIGQPRGKTVKLLRSFLKAGGEVIDSLTWHHYLYNGRTATREDPLN 304
Qy 313 PDVLDIFISSVQKVFQVVESTRPCKVWLGESTSAYGGAPLLSDTFAAGFMWLDKLGLS 372
Db 305 SDVLDTFILSVQKILKVTKEITPKKVKWLGESTSAYGGAPLLSDTFAAGFMWLDKLGLS 364
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Db 365 AQMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFKKLVGKVLMSVQSGSKRKL 424
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Db 425 VYLHCTNVYHPRYQEGDLTYLVNLNHNVTKYLKVPPLFRKPVDTYLLKPSGPDGLLSKS 484
Qy 493 VOLNGLTLKWVDDQTLPLMEKPLRPGSSILGPAFYSFFVIRNAKVAACI 543
Db 485 VOLNGQILKWVDEQTLPLTEKPLPAGSALSPLAFSYGFFVIRNAKVAACI 535

RESULT 6
Q6YGZ1_MOUSE
ID Q6YGZ1_MOUSE PRELIMINARY; PRT; 535 AA.
AC Q6YGZ1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heparanase.
GN Name=Hspe;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22841152; PubMed=12837765; DOI=10.1074/jbc.M300925200;
RA Gong F., Jemth P., Galvis M.L.E., Vlodavsky I., Horner A., Lindahl U.,

RA Li J.P.;
RL "Processing of macromolecular heparin by heparanase.";
RL J. Biol. Chem. 278:35152-35158(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Li J.-P., Gong F., Lindahl U.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY151051; AAN41636.1; -; mRNA.
DR MGI; MGI:1343124; Hspe.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); TAS.
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DR Pfam; PF03662; Glyco_hydro_79n; I.
SQ SEQUENCE 535 AA; 59992 MW; 374BAEB3795C718A CRC64;
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Best Local Similarity 76.8%; Pred. No. 1.4e-152;
Matches 408; Conservative 49; Mismatches 74; Indels 0; Gaps 0;
Qy 13 LMLLLGLPLSPGALPRPAQADVDLDFQTEPLHLVSPFLSVITDANLATDRPL 72
Db 5 LLLWLWGLGALAQAGAPAGTAPDDVVDLEFYTKRPLRSVSPFLSITIDASLATDRPL 64
Qy 73 ILLGSPKLRTLARGLSPAYLRFPGTKTDFELIFDPKKESTFEERSYQSQVNOQICKYGS 132
Db 65 TFLGSPRLRALARGLSPAYLRFPGTKTDFELIFDPKKESTFEERSYQSQVNOQICKYGS 124
Qy 133 PPDVEEKLRLWPYQEQALLREHYQKFKNSTYSSRSVDVLYTFPANCGLDLIFGLNALL 192
Db 125 SAAVLRKLVQEWPFQELLRLREYQKEFKNSTYSSRSVDVLYTFPANCGLDLIFGLNALL 184
Qy 193 RTADLQNSNAQALLDYCSSKGYNISWELGNPNFLKKADIPINGSQGLGEDFVLHKL 252
Db 185 RTPDLRWNSNAQALLDYCSSKGYNISWELGNPNFLKKADIPINGSQGLGEDFVLHKL 244
Qy 253 LRKSTFNKALYGPVQOPRRKTKAMLKSFKAGGEVIDSVTHHYLYNGRTATREDPLN 312
Db 245 LQSAFQNAKLYGPDIGQPRGKTVKLLRSFLKAGGEVIDSLTWHHYLYNGRTATREDPLN 304
Qy 313 PDVLDIFISSVQKVFQVVESTRPCKVWLGESTSAYGGAPLLSDTFAAGFMWLDKLGLS 372
Db 305 SDVLDTFILSVQKILKVTKEITPKKVKWLGESTSAYGGAPLLSDTFAAGFMWLDKLGLS 364
Qy 373 ARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFKKLVGKVLMSVQSGSKRKL 432
Db 365 AQMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFKKLVGKVLMSVQSGSKRKL 424
Qy 433 VYLHCTNTDPRYKEGDLTYALNHNVTKYLRLPYFNSKQVDKYLRLPLGPHGLLSKS 492
Db 425 VYLHCTNVYHPRYQEGDLTYLVNLNHNVTKYLKVPPLFRKPVDTYLLKPSGPDGLLSKS 484
Qy 493 VOLNGLTLKWVDDQTLPLMEKPLRPGSSILGPAFYSFFVIRNAKVAACI 543
Db 485 VOLNGQILKWVDEQTLPLTEKPLPAGSALSPLAFSYGFFVIRNAKVAACI 535

RESULT 7
Q7IRP1_RAT
ID Q7IRP1_RAT PRELIMINARY; PRT; 536 AA.
AC Q7IRP1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heparanase.
GN Name=Hspe; Synonyms=Hepe;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hulet M.D., Wang J., Hornby J.R., Freeman C., Pagler E., McHenry J.,
RA Parish C.R.;

```
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF359508; AAQ15189.1; -, mRNA.
DR RGD; 61969; Hpse.
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 536 AA; 60479 MW; C434E04CF536EA4D CRC64;

Query Match 75.3%; Score 2138; DB 2; Length 536;
Best Local Similarity 76.3%; Pred. No. 3.2e-152;
Matches 408; Conservative 49; Mismatches 78; Indels 0; Gaps 0;

Qy 9 LPPPLMLLLGPGSPGALPRPAQAQDVVDLDFFTQEPHLHVPSPFLSVTIDANLATD 68
Db 2 LRPLLLLWLWGRALALGALGCTAGTAPTKDVVDLDFYTKRLFQSPSPFLSVTIDASLATD 61
Qy 69 PRFLLILGSPKLRTLARGLSPAYLRFGGTKTDFLIDPKKESTFEERSYQSQVNQDICK 128
Db 62 PRFLTFLGSPRLRALARGLSPAYLRFGGTKTDFLIDPNKEPTSEERSYQSQVNNDICG 121
Qy 129 YGSIPDPVEEKLRLWEPYQEQILLREHYQKKFKNSTYSRSSVDVLYTFPANGSLDLIFGL 188
Db 122 SERVADVLRLKQWEPFQELLRLREYQREFKNSTYSRSSVDMLYSPAKCSRLDLIFGL 181
Qy 189 NALLRTADLWNSSNAQLLLDYCSSKGYNISWELGNENPSFLKKADIFINGSQGLGDFIQ 248
Db 182 NALLRTPDLRWNSSNAQLLLNYCSSKGYNISWELGNENPSFWKKAHISIDGLQGLGDFVE 241
Qy 249 LHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTHHHYLYNGRTATRE 308
Db 242 LHKLQKSAFQNAKLYGPDIGOPRGKTVKLLRSFLKAGGEVIDSLTWHHHYLYNGRVATKE 301
Qy 309 DFLNPVDLIDFISSQVKQFQVVESTRPGKKVWLGETSSAYGGAPLLSDTFAAGFMWLDK 368
Db 302 DFLSSDVLDTFILSVQKTLKVTKEMTPGKKVWLGETSSAYGGAPLLSDTFAAGFMWLDK 361
Qy 369 LGLSARMGIEVVMQRVFFGAGNYHLVDENPDPLDYWLSLLFKLVGPKVLMASVQSGKR 428
Db 362 LGLSAQLGIEVVMQRVFFGAGNYHLVDENFEPLDYWLSLLFKLVGPKVLMASVQSGPDR 421
Qy 429 RKLRYLHCTNTDNPYKEGDLTYAHLNHNVTKYLRLPYPFNSKNQVDKYLLRPLGPHGL 488
Db 422 SKLRVYLHCTNVHPRYREGDLTYVNLNHNVTKHLKLPMPFMRPVDKYLLKPFSGDGL 481
Qy 489 LSKSVQLNGTLKMWDDQTLPLMEKPLRPGSSSLGLPAFSYFVFVIRNAKVAACI 543
Db 482 LSKSVQLNGQTLKMWDEQTLPALTEKPLPAGSSLSVPAFSYGFFVIRNAKTAACI 536

RESULT 8
Q90ZF8_RAT PRELIMINARY; PRT; 536 AA.
AC Q90ZF8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Heparanase.
GN Name=Hpse; Synonyms=Hep;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22194309; PubMed=12077130; DOI=10.1074/jbc.M203282200;
RA Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita M.;
RT "Characterization of heparanase from a rat parathyroid cell line.";
RL J. Biol. Chem. 277:32459-32465 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Podyma K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita M.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF184967; AAF04563.1; -, mRNA.

DR RGD; 61969; Hpse.
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 536 AA; 60568 MW; 6208B1FD9EB28421 CRC64;

Query Match 74.8%; Score 2126; DB 2; Length 536;
Best Local Similarity 75.9%; Pred. No. 2.6e-151;
Matches 406; Conservative 50; Mismatches 79; Indels 0; Gaps 0;

Qy 9 LPPPLMLLLGPGSPGALPRPAQAQDVVDLDFFTQEPHLHVPSPFLSVTIDANLATD 68
Db 2 LRPLLLLWLWGRALALGCTAGTAPTKDVVDLDFYTKRLFQSPSPFLSVTIDASLATD 61
Qy 69 PRFLLILGSPKLRTLARGLSPAYLRFGGTKTDFLIDPKKESTFEERSYQSQVNQDICK 128
Db 62 PRFLTFLGSPRLRALARGLSPAYLRFGGTKTDFLIDPNKEPTSEERSYQSQVNNDICG 121
Qy 129 YGSIPDPVEEKLRLWEPYQEQILLREHYQKKFKNSTYSRSSVDVLYTFPANGSLDLIFGL 188
Db 122 SERVADVLRLKQWEPFQELLRLREYQREFKNSTYSRSSVDMLYSPAKCSRLDLIFGL 181
Qy 189 NALLRTADLWNSSNAQLLLDYCSSKGYNISWELGNENPSFLKKADIFINGSQGLGDFIQ 248
Db 182 NALLRTPDLRWNSSNAQLLLNYCSSKGYNISWELGNENPSFWKKAQISIDGLQGLGDFVE 241
Qy 249 LHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTHHHYLYNGRTATRE 308
Db 242 LHKLQKSAFQNAKLYGPDIGOPRGKTVKLLRSFLKAGGEVIDSLTWHHHYLYNGRVATKE 301
Qy 309 DFLNPVDLIDFISSQVKQFQVVESTRPGKKVWLGETSSAYGGAPLLSDTFAAGFMWLDK 368
Db 302 DFLSSDVLDTFILSVQKTLKVTKEMTPGKKVWLGETSSAYGGAPLLSDTFAAGFMWLDK 361
Qy 369 LGLSARMGIEVVMQRVFFGAGNYHLVDENPDPLDYWLSLLFKLVGPKVLMASVQSGKR 428
Db 362 LGLSAQLGIEVVMQRVFFGAGNYHLVDENFEPLDYWLSLLFKLVGPKVLMASVQSGPDR 421
Qy 429 RKLRYLHCTNTDNPYKEGDLTYAHLNHNVTKYLRLPYPFNSKNQVDKYLLRPLGPHGL 488
Db 422 SKLRVYLHCTNVHPRYREGDLTYVNLNHNVTKHLKLPMPFMRPVDKYLLKPFSGDGL 481
Qy 489 LSKSVQLNGTLKMWDDQTLPLMEKPLRPGSSSLGLPAFSYFVFVIRNAKVAACI 543
Db 482 LSKSVQLNGQTLKMWDEQTLPALTEKPLPAGSSLSVPAFSYGFFVIRNAKTAACI 536

RESULT 9
Q90YK5_CHICK PRELIMINARY; PRT; 523 AA.
AC Q90YK5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Heparanase.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21369959; PubMed=11387326; DOI=10.1074/jbc.M102462200;
RA Goldshmidt O., Zcharia E., Aingorn H., Guatta-Rangini Z., Azmon R.,
RA Michal I., Pecker I., Mitrani E., Vlodavsky I.;
RT "Expression pattern and secretion of human and chicken heparanase are
determined by their signal peptide sequence.";
RL J. Biol. Chem. 276:29178-29187 (2001).
DR EMBL; AY037007; AAK82648.1; -, mRNA.
DR Ensembl; ENSGALG0000011203; Gallus gallus.
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 523 AA; 58386 MW; 8EB0B7B18C9BF881 CRC64;
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Query Match 58.0%; Score 1648.5; DB 2; Length 523;
Best Local Similarity 60.3%; Pred. No. 2.4e-115;
Matches 321; Conservative 86; Mismatches 114; Indels 11; Gaps 3;

QY 13 LMLLLGLPLSPALPRPAQAQDVVDLDFFTQEPHLVSPSPFLSVTTIDANLATDPRFL 72
DB 2 LVLLLVLLVLAAPP-----RTAEQLQGLREPAGVSPFLSVTTIDANLATDPRFV 52
QY 73 ILLGSPKLRTLARGSPAYLRFGGTKTDFFLIDPKKSTFEERSYQSQVNQDICKYGS 132
DB 53 ALLRHPKLTLASGLSPGLRFGGTSTDFLIFNPKDSTWEEKVLSFQA-KOVCEAWPS 111
QY 133 PPVVEEKLRLBWPQOEQLLREHVKQKPKNSTYSSRSVDVLYTFANCGLDLPLGLNALL 192
DB 112 FAVVPKLLLTQWPLQEQKLLAEHSWKHKNTTITRSTLDILHTPASSSGFLRVFGLNALL 171
QY 193 RTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFKKADIFINGSCGCEPIQLHLK 252
DB 172 RRAGLQWSSNAQLLDYCAQRSYNIWELGNEPNSFKKSGICIDGFLGRDVFHLRQL 231
QY 253 L-RKSTFKNAKLYGPDVQPPRRKTAQMLKSPKAGGVEIDSVTWHHYLNGRTATREDFL 311
DB 232 LSQHPLYRHAELYGDPQPKHTQHLLRSEPKSGKAIDSVTWHHYVNGRSATREDFL 291
QY 312 NPVDLDFISVQVQVQVSTTRPGKVKWLGSTSSAYGGGAPLSDTFAAGFMWLDKGL 371
DB 292 SPEVLDSPATAIHDLVGLIVEATVPKKVWLGSTSSAYGGGAPLSDTFAAGFMWLDKGL 351
QY 372 SARMGIEVWQVFGAGNHLVDENFDPLDYHLISLFFKLYGKLVKVMASVQSKERKL 431
DB 352 AARGIDVWQVFGAGNHLVDENFDPLDYHLISLFFKLYGKLVKVMASVQSKERKL 411
QY 432 RVLHCTNTONPRYKEGDLTYAINLHNVTLPYFPGSKQVQVYKLLRPLGPHGLSK 491
DB 412 RVLHCTNPRPKYREGDVTLPALNLSVTQSLQPLKQSKSVQVQVYKLLRPLGPHGLSK 471
QY 492 SVQNLGLTKWDDQTLPLMEKPLRPGSSGLGPAFSPYFVIRNAKVAACI 543
DB 472 EVQNLGRLQWDDQTLPLHMAALAPGSTLGLPAPFSGYFVIRNAKVAACI 523

RESULT 10
Q4SYF6_TETNG
ID Q4SYF6_TETNG PRELIMINARY; PRT; 533 AA.
AC Q4SYF6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Chromosome undetermined SCAF12073, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0010356001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]

NUCLEOTIDE SEQUENCE.
RP Jallou O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Daillva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthonard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier C., Coutanceau J.P., Gouty J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."

Nature 431:946-957 (2004).
[2]
RL NUCLEOTIDE SEQUENCE.
RN Genoscope; Whitehead Institute Centre for Genome Research;
RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01012073; CAF94326.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 533 533
FT NON_TER 533 AA; 60100 MW; 9800A7C8780100FF CRC64;
SQ SEQUENCE 533 AA; 60100 MW; 9800A7C8780100FF CRC64;
Query Match 46.5%; Score 1320; DB 2; Length 533;
Best Local Similarity 50.2%; Pred. No. 1.4e-90;
Matches 269; Conservative 82; Mismatches 141; Indels 44; Gaps 8;

QY 49 LHLVSPFLSVTTIDANLATDPRFLILGSPKLTLAGLSPAYLRFGGTKTDFFLFPKK 108
DB 1 LRRVDRPFLSVTTIDASLAADERFMYLLSSPKVTLAKALTPAFLRFGTQDPMVPAPHK 60
QY 109 E---STFEERSYQSQVNQDICKYGSIPDPVEEKLRLWEVYQEQLLREHYQKFKNSTY 165
DB 61 NQPASGFSARELTFSSNGHSCCKMAPPPWLERRLKTEWKKQVQMLRNEELQRYRVKF 120
QY 166 SRSSVDVLYTFANCGLDLIFGLNALLRTADLQWSSNAQLLDYCSSKGYNISWELGNE 225
DB 121 TETTVQHLAFANCGLDLVFLNALLRTADLQWSSNAQLLDYCSSKGYNISWELGNE 180
QY 226 PNFLLKADIFINGSCGCEPIQLHLKLRKSTF-KNAKLYGPDVQPPRRKTAQMLKSLFK 284
DB 181 PNEYKAGLRLDGRQLGDEFTVLRKTLRESRYRDAGLFGPDVQPPRRKTAQMLKSLFK 240
QY 285 AGGEVDSVTWHHYLNGRTATREDFLNPDVLDIFISSVQKQVQVYKLLRPLGPHGLSK 344
DB 241 SGAEVADCTWHHYLNGRTATREDFLNPDVLDIFISSVQKQVQVYKLLRPLGPHGLSK 300
QY 345 SSAYGGGAPLSDTFAAGFMWLDKGLSARMGTEVWQVFFGAGNHYLVDENFDPLP-- 402
DB 301 SSAYGGGAPLSDTFAAGFMWLDKGLSARMGTEVWQVFFGAGNHYLVDENFDPLP-- 360
QY 403 -----DYWLSLLPKLVGTVKLVMA-----SVQSKRRKLRLVYLHCTNTDN----- 442
DB 361 GLLLDQWLSLLKLVGTVKLVGTVKLVGTVKLVGTVKLVGTVKLVGTVKLVGTVKLV 418
QY 443 -----PRYKEGDLTYAINLHNVTLPYFPGSKQVQVYKLLRPLGPHGLSK 487
DB 419 QRKEARFSLVSLCSYRSGAATLMSNLSKQAPRISLPRILSSSTVFAVLESEQP-GE 477
QY 488 LLSKSVQNLGLTKWDDQTLPLMEKPLRPGSSGLGPAFSPYFVIRNAKVAACI 543
DB 478 LRSRAVKNLGRVLRWDDQTLPLMEKPLRPGSSGLGPAFSPYFVIRNAKVAACI 533

RESULT 11
Q9H37_HUMAN
ID Q9H37_HUMAN PRELIMINARY; PRT; 592 AA.
AC Q9H37;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hepatanase-like protein HPA2c.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]

NUCLEOTIDE SEQUENCE.
RP MEDLINE=20483645; PubMed=11027606; DOI=10.1006/bbrc.2000.3586;
RA McKenzie E., Tyson K., Stamps A., Smith P., Turner P., Barry R.,
RA Hircok M., Patel S., Barry E., Stubbfield C., Terrett J., Page M.,
RT "Cloning and expression profiling of Hpa2, a novel mammalian


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QY 3 LRSKPALPPLMLLLGLPLSPGALPRPAQA-----QDVVDLDFQTEPLHLVSP 54
Db 16 LASLAALVLP--LVLSPPS--SSSTQRPVAGKRGPGFVETRLILLDVNTRSFIRVLD 71
QY 55 SFLSVTIDANLATPRFLILLGSPKRLTLARGLSPAYLRFGGTKTDFLIFDPKKE----- 109
Db 72 NFLSLQLDPSIIKD-GWLDLSSGLVTLARGLSPAFRLFGRKRTDFLQFTNQKNAKFR 130
QY 110 ---STFEERSYQSOVNQDI-----CKYGSIPDPVEEKRLERLWPFYQEQ-LLREHYQK 158
Db 131 GPGPDYLYKNEYDDIIRSDIALDKQKCKLAS-HPDMWLELQREKAASQTQVLLKEQLSN 189
QY 159 KFKNST----YSRS-----SDVLYTFANCGLDLIFGLNALRTADLQWNSNAQLLDY 210
Db 190 IYSNITLTGLFSHRIARSLSKLYNFADCGHLILGULNALHRPDPHSWNTSSTLSLKY 249
QY 211 CSSKGYNISWELGNEPNSFLKADIFINGSQGLDFIQLHKLRLK-STFKNAKLYGPDVG 269
Db 250 SAGKYNISWELGNEPNAYRSMVGHAVNSSQLAQDYTKRLTLQSVRYYSRAQLYGNAG 309
QY 270 QPRKTKAKWLSFLKAGGEVIDSVTHHHYLYNGRTATREDFLNPDVLDIFISSVQKVPQV 329
Db 310 RPRKNALLLDEFKMTGTGTVVDAVTHQHYMDGRIKKVEDEFLKRLDRLTLTEQLSKVTKV 369
QY 330 VESTRPGKVKWLGESTSSAYGGGAPLLSDTEAGFWMLDKGLSARMGIEVVNR---QVF 385
Db 370 VNTHTPGKVKWLGGLGPAWTGMSNLSDTFAGFLWVNTLGMWAAQGDVVLIRQAVQEH 429
QY 386 FGAGNYHLVDENFDP-LPDYWLSSLFLKVLGVTGKVLMSVQSGKR-----KLRYVL 435
Db 430 TNKQSVLFLQMFVPSFDPYFSLVFLKVLAVRAGLQKPGQRPQVIRDKLRIYA 489
QY 436 HCTNTDNPYKEGDTLTYAINLHNVTYKRLPYPPSPNKQVDKYLRLPLGPHGLLSKVQL 495
Db 490 HCTSNNHYVYRGSTIYIINLHRSRKKIKLAGTLRNIVHGYLLQPYGADGLRAKHVOL 549
QY 496 NGLTKWDDQTLPLMEKPRQSSGLPAFSYFFVIRNAKYAAC 542
Db 550 NGEKLLMADNETFPPELKPTLRAGTIAWPMTTIGFYVIRKINAYAC 596

RESULT 15
OSVUH4_HUMAN PRELIMINARY; PRT; 548 AA.
AC OSVUH4;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Heparanase 2.
GN Name=HPSE2; ORFNames=RP11-439D8.2-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Doggett S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Holt K.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Heath P.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
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RA Smith M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
Db EMBL; AL590036; CAH73139.1; -; Genomic DNA.
Db EMBL; AL356220; CAH17162.1; -; Genomic DNA.
Db EMBL; AL356268; CAH70450.1; -; Genomic DNA.
Db EMBL; AL445251; CAH16474.1; -; Genomic DNA.
Db EMBL; AL139243; CAH14148.1; -; Genomic DNA.
Db EMBL; AL139243; CAH73139.1; JOINED; Genomic DNA.
Db EMBL; AL356220; CAH73139.1; JOINED; Genomic DNA.
Db EMBL; AL445251; CAH73139.1; JOINED; Genomic DNA.
Db EMBL; AL356220; CAH14148.1; JOINED; Genomic DNA.
Db EMBL; AL445251; CAH14148.1; JOINED; Genomic DNA.
Db EMBL; AL356268; CAH17162.1; JOINED; Genomic DNA.
Db EMBL; AL590036; CAH17162.1; JOINED; Genomic DNA.
Db EMBL; AL445251; CAH70450.1; JOINED; Genomic DNA.
Db EMBL; AL356220; CAH70450.1; JOINED; Genomic DNA.
Db EMBL; AL356220; CAH16474.1; JOINED; Genomic DNA.
Db EMBL; AL356220; CAH16474.1; JOINED; Genomic DNA.
Db EMBL; AL39243; CAH70450.1; JOINED; Genomic DNA.
Db EMBL; AL445251; CAH70450.1; JOINED; Genomic DNA.
Db EMBL; AL39243; CAH70450.1; JOINED; Genomic DNA.
Db EMBL; AL445251; CAH17162.1; JOINED; Genomic DNA.
Db EMBL; AL39243; CAH17162.1; JOINED; Genomic DNA.
Db EMBL; AL590036; CAH14148.1; JOINED; Genomic DNA.
Db EMBL; AL356268; CAH14148.1; JOINED; Genomic DNA.
Db EMBL; AL356288; CAH73139.1; JOINED; Genomic DNA.
Db InterPro; IPR005199; Glyco_hydro_79_N.
Db Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 548 AA; 61816 MW; 2572C68423CD2C51 CRC64;

Query Match 35.8%; Score 1017.5; DB 2; Length 548;
Best Local Similarity 42.4%; Pred. No. 9.1e-68;
Matches 222; Conservative 78; Mismatches 171; Indels 53; Gaps 9;

QY 20 PLGLSPAL-----PRPA-----QAQDVVDLDFQTEPLHLVSPS 55
Db 18 PPACIAPGALYALALLHLSSQAGDRRLPVDRAGLKEKTLILLDVSTKQNVTVNEN 77
QY 56 FLSVTIDANLATPRFLILLGSPKRLTLARGLSPAYLRFGGTKTDFLIF-----DPKKEST 111
Db 78 FLSQLDPSIIHD-GWLDLSSKRLVTLARGLSPAFRLFGRKRTDFLQFQNLNRPASRG 136
QY 112 FEERSYQSOVNQDI-----CKYGSIPDPVEEKRLERLWPFYQEQ-LLREHYQK 158
Db 137 GPGPDYLYKNEYDDIIRSDVALDKQKCKIAQ-HPDMWLELQREKAQMHLVLLKEQFSN 195
QY 159 KFKNSTYSRGSVDVLYTFANCGLDLIFGLNALRTADLQWNSNAQLLDYCSKGYNI 218
Db 196 TYSNLTARSLDKLYNFADCSGLHLIFALNALRPNNSWSSALLKYSASKYNI 255
QY 219 SWEIENPNSFLKADIFINGSQGLDFIQLHKLRLK-STFKNAKLYGPDVGQPRKTKAK 277
Db 256 SWEIENPNNYRTWHEGRAVNSQLGKDYIQLKSLQPIRIYSRASLYGNIGRPRKNVIA 315
QY 278 MLKSFKAGGEVIDSVTHHHYLYNGRTATREDFLNPDVLDIFISSVQKVFQVSTPRGK 337
Db 316 LLDGFMKVGASTVDAVTWQHCVYIDGRVYVWMDFLKRLDRLTLSDQIRKIQVNTYTPGK 375
QY 338 KWLGETSSAYGGGAPLLSDTFAGFWMLDKGLSARMGIEVVNRQVFPFGAGNYHLVDEN 397
Db 376 KIWLEGVVTSAGGTNNLSDSYAGFLWNTLGMLANQSIDVIRHSFDDHGYNHLVDQN 435
QY 398 FDLPLDYWLSSLFLKVLGVTGKVLMSVQSGKR-----KLRYHLCTNTDNPYKEG 448
Db 436 FNPLPDYWLSSLYKRLIGPKVLAVHVAGLQKRPGRVIRDKLRIYACTNHHNHYVRG 495
QY 449 DLTLYAINLHNVTYKRLPYPPSPNKQVDKYLRLPLGPHGLLSKS 492
Db 496 SITLFIINLHRSRKKIKLAGTLRDKLVHGYLLQPYGQGLSKST 539
```

Search completed: February 27, 2006, 17:50:54

Job time : 236 secs



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OM protein - protein search, using sw model

Run on: February 27, 2006, 17:43:32 ; Search time 188 Seconds
(without alignments)

1269.057 Million cell updates/sec

Title: SEQ2-246PHE

Perfect score: 2841

Sequence: 1 MLRSKXPALPPLMLLLGP.....LPAFSYFFVIRNAKVAACI 543

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2841	100.0	543	2	Aay17082 Human hep
2	2841	100.0	543	4	Aab86206 Human hep
3	2841	100.0	543	7	Add18950 Human dis
4	2841	100.0	543	8	Adk52086 Human ato
5	2841	100.0	543	8	Adm48759 Human hpa
6	2841	100.0	543	8	Adn05074 Antipsori
7	2841	100.0	543	8	Adn04902 Antipsori
8	2841	100.0	543	8	Adq80372 Heparanas
9	2841	100.0	543	8	Adr88210 Human pre
10	2841	100.0	543	8	Adp25079 PRO poly
11	2841	100.0	543	8	Adt78177 Human hep
12	2841	100.0	543	9	Ady27036 Human hep
13	2841	100.0	543	9	Aea42426 Human hep
14	2841	100.0	588	2	Aay30124 A human p
15	2838	99.9	543	2	Aay02345 A human h
16	2838	99.9	543	3	Aay57590 Human hep
17	2838	99.9	543	3	Aab08849 Amino aci
18	2838	99.9	543	3	Aay52990 Human hep
19	2838	99.9	543	4	Aay97635 Human hep
20	2838	99.9	543	5	Abb07813 Human hep
21	2838	99.9	543	7	Adg88800 Human hpa
22	2838	99.9	543	8	Adl16379 Human hep
23	2838	99.9	543	8	Adm48716 Human hpa
24	2838	99.9	543	9	Aea42466 Human hep

25	2838	99.9	592	2	AAY02346	Aay02346 A human h
26	2838	99.9	592	3	AAB08850	Aab08850 Amino aci
27	2838	99.9	592	7	ADG88804	Adg88804 Human SK-
28	2838	99.9	592	8	ADL16383	Adl16383 Human hep
29	2838	99.9	592	8	ADM48720	Adm48720 Human SK-
30	2838	99.9	592	9	AEA42461	Aea42461 Human hep
31	2835	99.8	543	8	ADO63831	Ado63831 Human hep
32	2835	99.8	543	8	ADO63823	Ado63823 Human hep
33	2835	99.8	543	8	ADO63832	Ado63832 Human hep
34	2835	99.8	543	8	ADO63822	Ado63822 Human hep
35	2829	99.6	543	4	AAB88361	Aab88361 Human mem
36	2829	99.6	543	8	ADO63824	Ado63824 Human hep
37	2829	99.6	543	9	ADY63087	Ady63087 Human clo
38	2824.5	99.4	556	9	ADZ19010	Adz19010 Heparanas
39	2820	99.3	545	6	ABP56822	Abp56822 Human hep
40	2820	99.3	545	7	ADE16012	Adel16012 G-coupled
41	2820	99.3	545	8	ADL93951	Adl93951 Human G-c
42	2807.5	98.8	570	9	ADZ19008	Adz19008 Heparanas
43	2767	97.4	530	2	AAY34173	Aay34173 Human pre
44	2740	96.4	532	2	AAY17083	Aay17083 Seq ID No
45	2695	94.9	527	9	ADZ19004	Adz19004 HepGS4 co

ALIGNMENTS

RESULT 1
AAY17082
ID AAY17082 standard; protein; 543 AA.
XX AC AAY17082;
XX XX
XX 21-JUL-1999 (first entry)
XX XX
XX Human heparanase enzyme.
XX XX
XX Heparanase; endoglucuronidase; heparan sulfate proteoglycan; enzyme;
XX KW metastasis; angiogenesis; wound healing; angioplasty-induced restenosis;
XX KW arteriosclerosis; atherosclerosis; inflammation; tissue development;
XX KW human; HSPG.
XX OS Homo sapiens.
XX XX
XX FN WO9921975-A1.
XX XX
XX PD 06-MAY-1999.
XX XX
XX PF 28-OCT-1998; 98WO-AU000898.
XX XX
XX PR 28-OCT-1997; 97AU-00000062.
XX PR 09-DEC-1997; 97AU-00000812.
XX XX
XX PA (AUSU) UNIV AUSTRALIAN NAT.
XX XX
XX PI Freeman CG, Hulett MD, Parish CR, Hamdorf BJ;
XX XX
XX DR WPI; 1999-312956/26.
XX DR N-FSDB; AAX37259.
XX XX
XX PT Polynucleotides encoding mammalian endoglucuronidases, especially
XX XX heparanases, useful to promote wound healing.
XX XX
XX PS Claim 6; Page 69-73; 112pp; English.
XX XX
XX CC The invention relates to nucleic acid sequences that encode heparanase
XX CC enzymes having endoglucuronidase activity. Recombinant heparanases are
XX CC capable of removing the HS side chain from heparan sulfate proteoglycan
XX CC (HSPG). Sulfated oligosaccharides, sulphates or HSPG can be used to
XX CC inhibit heparanase, this is useful for treatment of a physiological or
XX CC medical condition associated with elevated heparanase activity, such as
XX CC metastasis, angiogenesis, wound healing, angioplasty-induced restenosis,
XX CC arteriosclerosis, atherosclerosis and inflammation. The human, murine and
XX CC rat heparanases can be used to enhance wound healing, especially

CC associated with tissue development and repair. The conditions mentioned
CC above can be diagnosed using specific antibodies, and also using primers
CC and probes specific for the heparanase polynucleotides. Other uses of the
CC heparanases include sequencing sulfated molecules such as HSPG. The
CC present sequence represents a human heparanase
XX
XX
SQ Sequence 543 AA;

Query Match 100.0%; Score 2841; DB 2; Length 543;
Best Local Similarity 100.0%; Pred. No. 3e-275;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKPALPPMLLLGPGSPGALPRPAQADVVDDFFTQEPHLHVPSPFLSVT 60
DB 1 MLRSKPALPPMLLLGPGSPGALPRPAQADVVDDFFTQEPHLHVPSPFLSVT 60

QY 61 IDANLATDPRFLILGSPKRLTARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSYMQS 120
DB 61 IDANLATDPRFLILGSPKRLTARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSYMQS 120

QY 121 QVNQDICKYGSIPPDVEEKLRLWPYQQLLREHYQKFKNSTYSRSSVDVLYTFPANC 180
DB 121 QVNQDICKYGSIPPDVEEKLRLWPYQQLLREHYQKFKNSTYSRSSVDVLYTFPANC 180

QY 181 GLDLIFGLNALRTADLOWNSSNAQLLLDYCSSKGYNISWELGNPNPSFLKKADIFINGS 240
DB 181 GLDLIFGLNALRTADLOWNSSNAQLLLDYCSSKGYNISWELGNPNPSFLKKADIFINGS 240

QY 241 QLGEDFIQLHKLRLKSTFNKAKLYGPDVGQPRRTAKMLKSFKAGGEVIDSVTWHYYL 300
DB 241 QLGEDFIQLHKLRLKSTFNKAKLYGPDVGQPRRTAKMLKSFKAGGEVIDSVTWHYYL 300

QY 301 NGRTATREDFLNPVDLIDFISVQKVQFVVESTTRPGKKVWLGETSAYGGAPLLSDTFA 360
DB 301 NGRTATREDFLNPVDLIDFISVQKVQFVVESTTRPGKKVWLGETSAYGGAPLLSDTFA 360

QY 361 AGFMWLDKLGLSARMGIEVVMQVFFGAGNYHLVDENFDPLDYWLSLLFKLVGTVKVL 420
DB 361 AGFMWLDKLGLSARMGIEVVMQVFFGAGNYHLVDENFDPLDYWLSLLFKLVGTVKVL 420

QY 421 ASVQGSKRRKLRLVYLHCTNTDNPRYKEGDLTLAYINLHNVTYKLYLPPYFSNKQVDKYL 480
DB 421 ASVQGSKRRKLRLVYLHCTNTDNPRYKEGDLTLAYINLHNVTYKLYLPPYFSNKQVDKYL 480

QY 541 ACT 543
DB 541 ACT 543

RESULT 2
AAB86206
ID AAB86206 standard; protein; 543 AA.
XX
AC AAB86206;
XX
DT 24-AUG-2001 (first entry)
XX
DE Human heparanase inhibitor protein.
XX
KW Heparanase; inhibitor; cardiac insufficiency; cardiact; nephrotropic;
KW hepatocytic; veterinary medicine; congestive heart failure; dyspnoea;
KW primary cardiomyopathy; peripheral odema; pulmonary congestion;
KW hepatic congestion; hydrothorax; ascite; nocturia; human.

OS Homo sapiens.
XX
XX DE19955803-A1.
XX
XX 23-MAY-2001.
PD

XX 19-NOV-1999; 99DE-01055803.
PF
XX 19-NOV-1999; 99DE-01055803.
PR
XX (KNOL) KNOLL AG.
PA
XX Herr D, Hahn A, Laux V;
PI
XX WPI; 2001-368371/39.
DR
DR N-PSDB; AAH20940.
XX
PT Treatment or prevention of cardiac insufficiency and related conditions,
PT e.g. pulmonary congestion and dyspnoea, comprises administration of
PT heparanase inhibitor.
XX
PS Disclosure; Page 11-13; 16pp; German.
XX
CC This invention describes a novel heparanase inhibitor which can be used
CC for the treatment or prevention of cardiac insufficiency and associated
CC indications, symptoms and/or malfunctions. The heparanase inhibitor of
CC the invention has cardiact, nephrotropic and hepatotropic activity. The
CC products of the invention can be used in human and veterinary medicine,
CC for the treatment or prevention of congestive heart failure e.g. primary
CC cardiomyopathy. Associated conditions treated or prevented with the
CC inhibitor are especially peripheral odemas, pulmonary and hepatic
CC congestion, dyspnoea, hydrothorax and ascites. Renal problems, e.g.
CC nocturia can also be treated. This sequence represents the human
CC heparanase protein described in the method of the invention
XX
SQ Sequence 543 AA;

Query Match 100.0%; Score 2841; DB 4; Length 543;
Best Local Similarity 100.0%; Pred. No. 3e-275;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKPALPPMLLLGPGSPGALPRPAQADVVDDFFTQEPHLHVPSPFLSVT 60
DB 1 MLRSKPALPPMLLLGPGSPGALPRPAQADVVDDFFTQEPHLHVPSPFLSVT 60

QY 61 IDANLATDPRFLILGSPKRLTARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSYMQS 120
DB 61 IDANLATDPRFLILGSPKRLTARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSYMQS 120

QY 121 QVNQDICKYGSIPPDVEEKLRLWPYQQLLREHYQKFKNSTYSRSSVDVLYTFPANC 180
DB 121 QVNQDICKYGSIPPDVEEKLRLWPYQQLLREHYQKFKNSTYSRSSVDVLYTFPANC 180

QY 181 GLDLIFGLNALRTADLOWNSSNAQLLLDYCSSKGYNISWELGNPNPSFLKKADIFINGS 240
DB 181 GLDLIFGLNALRTADLOWNSSNAQLLLDYCSSKGYNISWELGNPNPSFLKKADIFINGS 240

QY 241 QLGEDFIQLHKLRLKSTFNKAKLYGPDVGQPRRTAKMLKSFKAGGEVIDSVTWHYYL 300
DB 241 QLGEDFIQLHKLRLKSTFNKAKLYGPDVGQPRRTAKMLKSFKAGGEVIDSVTWHYYL 300

QY 301 NGRTATREDFLNPVDLIDFISVQKVQFVVESTTRPGKKVWLGETSAYGGAPLLSDTFA 360
DB 301 NGRTATREDFLNPVDLIDFISVQKVQFVVESTTRPGKKVWLGETSAYGGAPLLSDTFA 360

QY 361 AGFMWLDKLGLSARMGIEVVMQVFFGAGNYHLVDENFDPLDYWLSLLFKLVGTVKVL 420
DB 361 AGFMWLDKLGLSARMGIEVVMQVFFGAGNYHLVDENFDPLDYWLSLLFKLVGTVKVL 420

QY 421 ASVQGSKRRKLRLVYLHCTNTDNPRYKEGDLTLAYINLHNVTYKLYLPPYFSNKQVDKYL 480
DB 421 ASVQGSKRRKLRLVYLHCTNTDNPRYKEGDLTLAYINLHNVTYKLYLPPYFSNKQVDKYL 480

QY 481 RPLGPHGLLSKSVQNLNGLTLKMVDQDTLPLMEKPLRPGSSLGLPFASYSFFVIRNAKVA 540
DB 481 RPLGPHGLLSKSVQNLNGLTLKMVDQDTLPLMEKPLRPGSSLGLPFASYSFFVIRNAKVA 540

QY 541 ACT 543

```

Db      541 ACI 543

RESULT 3
ADD18950
ID ADD18950 standard; protein; 543 AA.
XX
AC ADD18950;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human disease related protein SeqID439.
XX
KW human; disease state; cytostatic; antiinflammatory; ophthalmological;
KW antiarteriosclerotic; vulnary; gene therapy;
KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
KW glucose transportation; catecholamine synthesis; iron transport;
KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
KW inflammatory condition; wound healing.
XX
OS Homo sapiens.
XX
FN WO2003018621-A2.
XX
PD 06-MAR-2003.
XX
PF 23-AUG-2002; 2002WO-GB003892.
XX
PR 23-AUG-2001; 2001GB-00020558.
XX
PR 05-OCT-2001; 2001GB-00024037.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
XX
DR WPI; 2003-290046/28.
XX
DR N-PSDB; ADD18951.
XX
PT New substantially purified polypeptide, useful for diagnosing or treating
PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
PT wound healing.
XX
PS Claim 25; SEQ ID NO 439; 424pp; English.
XX
CC This invention relates to novel human genes and gene product which are
CC implicated in certain disease states. Compounds which modulate the
CC proteins of the invention may have cytostatic, antiinflammatory,
CC ophthalmological, antiarteriosclerotic or vulnerary activities. The
CC sequences of the invention may be useful for gene therapy. The invention
CC may be useful for diagnosing or treating a hypoxia-regulated condition,
CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
CC erythropoiesis, or the biological response to hypoxia conditions
CC including processes such as glycolysis, gluconeogenesis, glucose
CC transportation, catecholamine synthesis, iron transport or nitric oxide
CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
CC inflammatory conditions or wound healing. The present sequence is that of
CC a disease related protein of the invention.
XX
SQ Sequence 543 AA;

Query Match      100.0%; Score 2841; DB 7; Length 543;
Best Local Similarity 100.0%; Pred. No. 3e-275;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLRSKALPPPLMLLLGLPLSPGALPRPAQADVDLDFFTQBLHVSFSLVT 60
Db      1 MLRSKALPPPLMLLLGLPLSPGALPRPAQADVDLDFFTQBLHVSFSLVT 60

```


XX PS Example 2; SEQ ID NO 119; 484pp; Japanese.

XX CC The invention relates to detecting atopic dermatitis or psoriasis

CC comprising assaying the levels of expression of an indicator gene at a

CC rash site and non-rash site of a person with atopic dermatitis or

CC psoriasis, comparing these levels with those of a healthy person, and

CC determining that if the levels of indicators are higher or lower, then

CC this indicates the disease. Also included are a reagent for detecting

CC atopic dermatitis or psoriasis, a kit for screening for treatments, a

CC transgenic non human vertebrate animal models for the diseases, an agent

CC for inducing the diseases in mice and a DNA chip for assaying for the

CC indicator genes. The method is used for treatment, detection and animal

CC models for research of atopic dermatitis and psoriasis. The present

CC sequence is a protein encoded by an indicator gene of the invention.

XX SQ Sequence 543 AA;

Query Match 100.0%; Score 2841; DB 8; Length 543;

Best Local Similarity 100.0%; Pred. No. 3e-275;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLRSKPALPPPLMLLLGLGPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLVT 60

Db 1 MLLRSKPALPPPLMLLLGLGPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLVT 60

QY 61 IDANLATDPRFLLILGSPKRLTARGLSPAYLRFGGTKTDFLIDFPKKESTFEERSYQWS 120

Db 61 IDANLATDPRFLLILGSPKRLTARGLSPAYLRFGGTKTDFLIDFPKKESTFEERSYQWS 120

QY 121 QVNQDICKYGSIPDPVEEKLRLWEPYQEQLLREHYQKFKNSTYRSRSDVLYTFANCS 180

Db 121 QVNQDICKYGSIPDPVEEKLRLWEPYQEQLLREHYQKFKNSTYRSRSDVLYTFANCS 180

QY 181 GLDLIFGLNALLRTADLQWSSNAQLLDYCSSKGYNISWELGNENPSFLKKADIFINGS 240

Db 181 GLDLIFGLNALLRTADLQWSSNAQLLDYCSSKGYNISWELGNENPSFLKKADIFINGS 240

QY 301 NGRTATREDFLNPDLVDLFISSQVKVFQVVESTPGKKVWLGETSSAYGCGAPLLSDTFA 360

Db 301 NGRTATREDFLNPDLVDLFISSQVKVFQVVESTPGKKVWLGETSSAYGCGAPLLSDTFA 360

QY 361 AGFMWLDKLGSLARMGIEVVMRGVFFGAGNYHLVDENFDPLPDYWLSSLFKLVGTKVLM 420

Db 361 AGFMWLDKLGSLARMGIEVVMRGVFFGAGNYHLVDENFDPLPDYWLSSLFKLVGTKVLM 420

QY 421 ASVQSGSKRRKRLRYLHCTNTDPRYKEGDLTLVAINLHNVTKYLRPLYPFSNKQVDKYL 480

Db 421 ASVQSGSKRRKRLRYLHCTNTDPRYKEGDLTLVAINLHNVTKYLRPLYPFSNKQVDKYL 480

QY 481 RPLGPHGLSKSVQLNGLTLKWDDQTLPLPEKPLRPGSSGLPAPFSYFFVIRNAKVA 540

Db 481 RPLGPHGLSKSVQLNGLTLKWDDQTLPLPEKPLRPGSSGLPAPFSYFFVIRNAKVA 540

QY 541 ACI 543

Db 541 ACI 543

RESULT 5

ADM48759

ID ADM48759 standard; protein; 543 AA.

XX AC

XX AC ADM48759;

XX DT 03-JUN-2004 (first entry)

XX DE Human hpa protein #2.

XX

KW Transgenic animal; heparanase; cancer; viral infection; restenosis;

KW neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa;

KW human.

XX Homo sapiens.

OS US2003217375-A1.

PN 20-NOV-2003.

XX 24-FEB-2003; 2003US-00371218.

XX 31-AUG-1998; 98WO-US017954.

PR 01-MAR-1999; 99US-00258892.

PR 06-FEB-2001; 2001US-00776874.

PR 19-NOV-2001; 2001US-00988113.

XX (ZCHA/) ZCHARIA E.

PA (VLOD/) VLODAVSKY I.

PA (METZ/) METZGER S.

PA (PECK/) PECKER I.

PA (ILAN/) ILAN N.

PA (CHAJ/) CHAJEK-SHAUL T.

PA (GOLD/) GOLDSHMIDT O.

XX Zcharia E, Vlodavsky I, Metzger S, Pecker I, Ilan N;

PI Chajek-Shaul T, Goldshmidt O;

DR WPI; 2004-021918/02.

DR N-PSDB; ADM48748.

XX New transgenic non-human animal expressing heparinase, useful as models

PT for human disease, such as cancers, viral infection, neurodegenerative

PT diseases, restenosis, atherosclerosis and pulmonary disorders.

XX Example 10; Fig 16; 106pp; English.

PS The present invention relates to a transgenic non-human animal whose

CC genome comprises an exogenous polynucleotide sequence, including a

CC promoter active in tissues of the non-human, a region encoding a human

CC heparanase, where the promoter and the region encoding human heparanase

CC are operably linked in the exogenous polynucleotide such that human

CC heparanase is expressed in at least a portion of the cells of the non-

CC human animal. The methods and compositions of the present invention are

CC useful for the production of transgenic animals expressing heparanase, to

CC be used as models for human diseases such as cancers, viral infection,

CC restenosis, neurodegenerative diseases, atherosclerosis and pulmonary

CC disorders. The present sequence is human hpa protein used in the

CC exemplification of the invention.

XX SQ Sequence 543 AA;

Query Match 100.0%; Score 2841; DB 8; Length 543;

Best Local Similarity 100.0%; Pred. No. 3e-275;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLRSKPALPPPLMLLLGLGPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLVT 60

Db 1 MLLRSKPALPPPLMLLLGLGPGALPRPAQAQDVVDLDFFTQEPHLHVSFSLVT 60

QY 61 IDANLATDPRFLLILGSPKRLTARGLSPAYLRFGGTKTDFLIDFPKKESTFEERSYQWS 120

Db 61 IDANLATDPRFLLILGSPKRLTARGLSPAYLRFGGTKTDFLIDFPKKESTFEERSYQWS 120

QY 121 QVNQDICKYGSIPDPVEEKLRLWEPYQEQLLREHYQKFKNSTYRSRSDVLYTFANCS 180

Db 121 QVNQDICKYGSIPDPVEEKLRLWEPYQEQLLREHYQKFKNSTYRSRSDVLYTFANCS 180

QY 181 GLDLIFGLNALLRTADLQWSSNAQLLDYCSSKGYNISWELGNENPSFLKKADIFINGS 240

Db 181 GLDLIFGLNALLRTADLQWSSNAQLLDYCSSKGYNISWELGNENPSFLKKADIFINGS 240

QY 241 QLGEDFIQLHKLARKSTFFKNALYGPDPVGPQRKRTAKMLKSLFKAGEVIDSVTWHYYL 300

Db 241 QLGEDFIQLHLLRSTFKNAKLYGPDVQPRRTAKMLKSPFKAGGEVIDSVTWHYYL 300
QY 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTRPKKVLGGETSSAYGGGAPLLSDTFA 360
Db 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTRPKKVLGGETSSAYGGGAPLLSDTFA 360
QY 361 AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFVKLVGTVLM 420
Db 361 AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFVKLVGTVLM 420
QY 421 ASVOGSKRRKLRVYLHCTNTDNPYKEGDLTYAINLHNVTYILPYPFSNKQVDKYL 480
Db 421 ASVOGSKRRKLRVYLHCTNTDNPYKEGDLTYAINLHNVTYILPYPFSNKQVDKYL 480
QY 481 RPLGPHGLLSKSVQNLGLTLKMVDDQTLPLMEKPLRPGSSLGLPAPFSYSPFVIRNAKVA 540
Db 481 RPLGPHGLLSKSVQNLGLTLKMVDDQTLPLMEKPLRPGSSLGLPAPFSYSPFVIRNAKVA 540
QY 541 ACI 543
Db 541 ACI 543

RESULT 6
ADN05074
ID ADN05074 standard; protein; 543 AA.

AC ADN05074;
DT 01-JUL-2004 (first entry)
DE Antipsoriatic protein sequence #716.
KW antipsoriatic; gene therapy; psoriasis; diagnosis.

OS Homo sapiens.

FN WO2004028479-A2.

PD 08-APR-2004.

PF 25-SEP-2003; 2003WO-US030907.

PR 25-SEP-2002; 2002US-0414006P.

PA (GETH) GENENTECH INC.

PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;

XX WPI; 2004-305105/28.

XX N-PSDB; ADN05073.

XX New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.

PS Claim 9; SEQ ID NO 1468; 3069pp; English.

XX The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.

XX Sequence 543 AA;

Query Match 100.0%; Score 2841; DB 8; Length 543;

Best Local Similarity 100.0%; Pred. No. 3e-275;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLRSKPALPPPLMLLLGLPLSPGALPRPAQADVVLDLFFFTQEPHLVSPSFLSVT 60

Db 1 MLLRSKPALPPPLMLLLGLPLSPGALPRPAQADVVLDLFFFTQEPHLVSPSFLSVT 60
QY 61 IDANLATDPRFLILLLGSPKRLTARGLSPAYLRFQGTKTDFLI FPKKKESTFEERSYWS 120
Db 61 IDANLATDPRFLILLLGSPKRLTARGLSPAYLRFQGTKTDFLI FPKKKESTFEERSYWS 120
QY 121 QVNODICKYGSIPPDVEEKLRLWPYQQLLLREHYQKKFNSTYSRSSVDVLYTFANCS 180
Db 121 QVNODICKYGSIPPDVEEKLRLWPYQQLLLREHYQKKFNSTYSRSSVDVLYTFANCS 180
QY 181 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNPNFSLKKADIFINGS 240
Db 181 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNPNFSLKKADIFINGS 240
QY 241 QLGEDFIQLHLLRSTFKNAKLYGPDVQPRRTAKMLKSPFKAGGEVIDSVTWHYYL 300
Db 241 QLGEDFIQLHLLRSTFKNAKLYGPDVQPRRTAKMLKSPFKAGGEVIDSVTWHYYL 300
QY 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTRPKKVLGGETSSAYGGGAPLLSDTFA 360
Db 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTRPKKVLGGETSSAYGGGAPLLSDTFA 360
QY 361 AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFVKLVGTVLM 420
Db 361 AGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFVKLVGTVLM 420
QY 421 ASVOGSKRRKLRVYLHCTNTDNPYKEGDLTYAINLHNVTYILPYPFSNKQVDKYL 480
Db 421 ASVOGSKRRKLRVYLHCTNTDNPYKEGDLTYAINLHNVTYILPYPFSNKQVDKYL 480
QY 481 RPLGPHGLLSKSVQNLGLTLKMVDDQTLPLMEKPLRPGSSLGLPAPFSYSPFVIRNAKVA 540
Db 481 RPLGPHGLLSKSVQNLGLTLKMVDDQTLPLMEKPLRPGSSLGLPAPFSYSPFVIRNAKVA 540
QY 541 ACI 543
Db 541 ACI 543

RESULT 7

ADN04902

ID ADN04902 standard; protein; 543 AA.

AC ADN04902;

DT 01-JUL-2004 (first entry)

DE Antipsoriatic protein sequence #631.

KW antipsoriatic; gene therapy; psoriasis; diagnosis.

XX Homo sapiens.

XX WO2004028479-A2.

PD 08-APR-2004.

PF 25-SEP-2003; 2003WO-US030907.

PR 25-SEP-2002; 2002US-0414006P.

PA (GETH) GENENTECH INC.

PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;

XX WPI; 2004-305105/28.

XX N-PSDB; ADN04901.

XX New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.

```
XX PS Claim 9; SEQ ID NO 1296; 3069pp; English.
XX CC The invention relates to novel polynucleotide and polypeptides for
XX CC treating psoriasis or a sequence having at least 80% identity to the
XX CC above sequences. The nucleic acid is useful for preparing a composition
XX CC for diagnosing or treating psoriasis in a mammal. This sequence
XX CC corresponds to one of the polypeptides of the invention.
XX SQ Sequence 543 AA;

Query Match 100.0%; Score 2841; DB 8; Length 543;
Best Local Similarity 100.0%; Pred. No. 3e-275;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLRSKPALPPMLLLGPGPLSPGALPRPAQADVVLDLFFFTQEPHLHVSFSLVT 60
Db 1 MLRSKPALPPMLLLGPGPLSPGALPRPAQADVVLDLFFFTQEPHLHVSFSLVT 60

Qy 61 IDANLATDPRFLLIGSPKRLTLARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSYQWS 120
Db 61 IDANLATDPRFLLIGSPKRLTLARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSYQWS 120

Qy 121 QVNQDICKYGSIPDPVEEKLRLWPYQEQALLREHYQKFKNSTYRSRSDVLYTFANCS 180
Db 121 QVNQDICKYGSIPDPVEEKLRLWPYQEQALLREHYQKFKNSTYRSRSDVLYTFANCS 180

Qy 181 GLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Db 181 GLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240

Qy 241 QLGEDFIQLHKLRLKSTFNNAKLYGPDVGQPPRRKTAKMLKSLFKAGGEVIDSVTHHHYL 300
Db 241 QLGEDFIQLHKLRLKSTFNNAKLYGPDVGQPPRRKTAKMLKSLFKAGGEVIDSVTHHHYL 300

Qy 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTPRGKVKWLGETSSAYGGAPLLSDTFA 360
Db 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTPRGKVKWLGETSSAYGGAPLLSDTFA 360

Qy 361 AGFMWLDKLGLSARMGIEVVMQVFFGAGNYHLVDENFDLPDYWLSLLFKLVGTKVLM 420
Db 361 AGFMWLDKLGLSARMGIEVVMQVFFGAGNYHLVDENFDLPDYWLSLLFKLVGTKVLM 420

Qy 421 ASVQSKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRPLPYFSPNKQVDKYL 480
Db 421 ASVQSKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRPLPYFSPNKQVDKYL 480

Qy 421 ASVQSKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRPLPYFSPNKQVDKYL 480
Db 421 ASVQSKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRPLPYFSPNKQVDKYL 480
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PD 29-JUL-2004.
XX 08-JAN-2004; 2004WO-US000368.
XX 08-JAN-2003; 2003US-0438735P.
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX Amler LC, Januario T;
XX WPI; 2004-544114/52.
XX N-PSDB; ADQ80253.
XX Identifying a mammal that will respond therapeutically to a method of
XX treating cancer comprises comparing the level of a biomarker in a mammal
XX before and after exposure to an epidermal growth factor receptor (EGFR)
XX modulator.
XX Disclosure; SEQ ID NO 144; 520pp; English.
XX The invention relates to a method of identifying a mammal that will
XX respond therapeutically to a method of treating cancer by administering
XX an epidermal growth factor receptor (EGFR) modulator by comparing the
XX level of a biomarker in a mammal before and after exposure to an EGFR
XX modulator. The method comprises: (a) measuring, in the mammal, the level
XX of at least one biomarker identified in the specification; (b) exposing
XX the mammal to the EGFR modulator; and (c) measuring in the mammal the
XX level of the biomarker, where a difference in the level in step (c)
XX compared to step (a) indicates that the mammal will respond
XX therapeutically to the method of treating cancer. The method and
XX biomarkers are useful for identifying a mammal that will respond
XX therapeutically to a method of treating cancer by administering an
XX epidermal growth factor receptor (EGFR) modulator. This sequence
XX corresponds to one of the biomarkers whose levels of expression is
XX measured in the method of the invention.
XX SQ Sequence 543 AA;

Query Match 100.0%; Score 2841; DB 8; Length 543;
Best Local Similarity 100.0%; Pred. No. 3e-275;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLRSKPALPPMLLLGPGPLSPGALPRPAQADVVLDLFFFTQEPHLHVSFSLVT 60
Db 1 MLRSKPALPPMLLLGPGPLSPGALPRPAQADVVLDLFFFTQEPHLHVSFSLVT 60

Qy 61 IDANLATDPRFLLIGSPKRLTLARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSYQWS 120
Db 61 IDANLATDPRFLLIGSPKRLTLARGLSPAYLRFGGTKTDFLI FDPKKESTFEERSYQWS 120

Qy 121 QVNQDICKYGSIPDPVEEKLRLWPYQEQALLREHYQKFKNSTYRSRSDVLYTFANCS 180
Db 121 QVNQDICKYGSIPDPVEEKLRLWPYQEQALLREHYQKFKNSTYRSRSDVLYTFANCS 180

Qy 181 GLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Db 181 GLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240

Qy 241 QLGEDFIQLHKLRLKSTFNNAKLYGPDVGQPPRRKTAKMLKSLFKAGGEVIDSVTHHHYL 300
Db 241 QLGEDFIQLHKLRLKSTFNNAKLYGPDVGQPPRRKTAKMLKSLFKAGGEVIDSVTHHHYL 300

Qy 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTPRGKVKWLGETSSAYGGAPLLSDTFA 360
Db 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTPRGKVKWLGETSSAYGGAPLLSDTFA 360

Qy 361 AGFMWLDKLGLSARMGIEVVMQVFFGAGNYHLVDENFDLPDYWLSLLFKLVGTKVLM 420
Db 361 AGFMWLDKLGLSARMGIEVVMQVFFGAGNYHLVDENFDLPDYWLSLLFKLVGTKVLM 420

Qy 421 ASVQSKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRPLPYFSPNKQVDKYL 480
Db 421 ASVQSKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYLRPLPYFSPNKQVDKYL 480
```


Db 181 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNFNSFLKKADIFINGS 240
QY 241 QLGEDFIQLHKLRLKSTFKNAKLYGPDVQVQPRRTAKMLKSFLLKAGGVIDSVTHHYYL 300
Db 241 QLGEDFIQLHKLRLKSTFKNAKLYGPDVQVQPRRTAKMLKSFLLKAGGVIDSVTHHYYL 300
QY 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRGKKVWLGTSAYGGAPLLSDTFA 360
Db 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRGKKVWLGTSAYGGAPLLSDTFA 360
QY 361 AGFMWLDKLGLSARMGIEVVMQVFFGAGNYHLVDENFDPLDYWLSLLFKKLVGTVKVL 420
Db 361 AGFMWLDKLGLSARMGIEVVMQVFFGAGNYHLVDENFDPLDYWLSLLFKKLVGTVKVL 420
QY 421 ASVQGSKRRKRLRVYLHCTNTDNPYKEGDLTIYALNHNVTYKLRPLPYFNSKNQVDKYL 480
Db 421 ASVQGSKRRKRLRVYLHCTNTDNPYKEGDLTIYALNHNVTYKLRPLPYFNSKNQVDKYL 480
QY 481 RPLGPHGLLSKSVQLNGLTLKWDDQTLPLMEKPLRPGSSLGLPAPFSYFFVIRNAKVA 540
Db 481 RPLGPHGLLSKSVQLNGLTLKWDDQTLPLMEKPLRPGSSLGLPAPFSYFFVIRNAKVA 540
QY 541 ACI 543
Db 541 ACI 543
RESULT 10
ADP25079
ID ADP25079 standard; protein; 543 AA.
XX
AC ADP25079;
XX
DT 18-NOV-2004 (first entry)
XX
DE PRO polypeptide SEQ ID NO:2257.
XX
KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
XX
OS Unidentified.
XX
PN WO2004041170-A2.
XX
PD 21-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-US034312.
XX
PR 01-NOV-2002; 2002US-0423394P.
XX
PA (GETH) GENENTECH INC.
XX
PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;
XX
DR WPI; 2004-419628/39.
DR N-PSDB; ADP25078.
XX
XX New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
PS Claim 7; SEQ ID NO 2257; 2940pp; English.
XX
XX The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antirheumatic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the

CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polynuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polynuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, Gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.
XX
SQ Sequence 543 AA;
Query Match 100.0%; Score 2841; DB 8; Length 543;
Best Local Similarity 100.0%; Pred. No. 3e-275;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLRSKPALPPMLMLLLGPLGSPGALPRPAQADVVLDLDFQTEPLHLVSPSFLSVT 60
Db 1 MLLRSKPALPPMLMLLLGPLGSPGALPRPAQADVVLDLDFQTEPLHLVSPSFLSVT 60
QY 61 IDANLATDPRFLIILGSPKRLTLARGLSPAYLRFQGTGTDLIIDPKKESFEERSYWS 120
Db 61 IDANLATDPRFLIILGSPKRLTLARGLSPAYLRFQGTGTDLIIDPKKESFEERSYWS 120
QY 121 QVNQDICKYGSIPDPDVEEKLRLWEPYQQLLREHYQKFKNSTYSRSSVDVLYTFANC 180
Db 121 QVNQDICKYGSIPDPDVEEKLRLWEPYQQLLREHYQKFKNSTYSRSSVDVLYTFANC 180
QY 181 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNFNSFLKKADIFINGS 240
Db 181 GLDLIFGLNALLRTADLQWNSNAQLLLDYCSSKGYNISWELGNFNSFLKKADIFINGS 240
QY 241 QLGEDFIQLHKLRLKSTFKNAKLYGPDVQVQPRRTAKMLKSFLLKAGGVIDSVTHHYYL 300
Db 241 QLGEDFIQLHKLRLKSTFKNAKLYGPDVQVQPRRTAKMLKSFLLKAGGVIDSVTHHYYL 300
QY 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRGKKVWLGTSAYGGAPLLSDTFA 360
Db 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRGKKVWLGTSAYGGAPLLSDTFA 360
QY 361 AGFMWLDKLGLSARMGIEVVMQVFFGAGNYHLVDENFDPLDYWLSLLFKKLVGTVKVL 420
Db 361 AGFMWLDKLGLSARMGIEVVMQVFFGAGNYHLVDENFDPLDYWLSLLFKKLVGTVKVL 420
QY 421 ASVQGSKRRKRLRVYLHCTNTDNPYKEGDLTIYALNHNVTYKLRPLPYFNSKNQVDKYL 480
Db 421 ASVQGSKRRKRLRVYLHCTNTDNPYKEGDLTIYALNHNVTYKLRPLPYFNSKNQVDKYL 480
QY 481 RPLGPHGLLSKSVQLNGLTLKWDDQTLPLMEKPLRPGSSLGLPAPFSYFFVIRNAKVA 540
Db 481 RPLGPHGLLSKSVQLNGLTLKWDDQTLPLMEKPLRPGSSLGLPAPFSYFFVIRNAKVA 540
QY 541 ACI 543
Db 541 ACI 543
RESULT 11
ADT78177
ID ADT78177 standard; protein; 543 AA.
XX
XX ADT78177;
AC

XX 13-JAN-2005 (first entry)
 XX Human heparanase protein.
 XX
 KW Antibody; epitope; heparanase; pathological condition; angiogenesis;
 KW cell proliferation; cancerous condition; tumour cell invasion;
 KW metastatic disease; heparanase-related disorder; inflammatory disorder;
 KW wound; scar; vasculopathy; autoimmune condition; renal disease;
 KW cytostatic; antiinflammatory; vulnery; antiarteriosclerotic;
 KW vasotropic; immunosuppressive; nephrotropic; antidiabetic; human.
 XX: Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Binding-site 157..162
 FT /note= "Putative heparin binding site"
 FT Binding-site 271..277
 FT /note= "Putative heparin binding site"
 FT Binding-site 426..433
 FT /note= "Putative heparin binding site"
 XX
 XX US2004213789-A1.
 XX
 XX 28-OCT-2004.
 PD
 XX 22-AUG-2003; 2003US-00645659.
 XX
 XX 02-SEP-1997; 97US-009221170.
 PR
 XX 01-MAY-1998; 98US-00071739.
 PR
 XX 04-NOV-1998; 98US-00186200.
 PR
 XX 19-FEB-2003; 2003US-00368044.
 XX
 XX (YACOBY-ZEEVI O.
 PA (PERE) PERETZ T.
 PA (MIRO) MIRON D.
 PA (SHLO) SHLOMI Y.
 PA (PECK) PECKER I.
 PA (AYAL) AYAL-HERSHKOVITZ M.
 PA (FEIN) FEINSTEIN E.
 PA (GELD) GELDER J M V.
 PA (VLOD) VLODAVSKY I.
 PA (FRIE) FRIEDMANN Y.
 XX
 XX Yacoby-Zeevi O, Peretz T, Miron D, Shlomi Y, Pecker I;
 PI Ayal-Hershkovitz M, Feinstein E, Gelder JMW, Vlodavsky I;
 PI Friedmann Y;
 XX
 XX WPI; 2004-774790/76.
 DR
 XX New neutralizing monoclonal anti-heparanase antibodies, useful for
 PT detecting, treating or preventing cancer, inflammatory or autoimmune
 PT disorder, wound, atherosclerosis, restenosis, or diabetic nephropathy.
 PT
 XX Claim 5; SEQ ID NO 4; 68pp; English.
 FS
 XX The invention relates to an isolated antibody or antibody portion capable
 CC of specifically binding to or elicited by at least one epitope of a
 CC heparanase protein, where the heparanase protein is at least 60%
 CC homologous to any of the 6 sequences given as SEQ ID NOS: 1-5 or 11, and
 CC where at least one epitope comprises a sequence at least 70% homologous
 CC to any of the sequences given as SEQ ID NOS: 6-10. Also disclosed are (a)
 CC a hybridoma cell line comprising a cell line for producing the monoclonal
 CC antibody, (b) a method for detecting, treating or preventing a
 CC pathological condition or a heparanase-related disorder or condition in a
 CC subject, (c) a method for monitoring the state of a heparanase-related
 CC disorder or condition in a subject, and (d) a pharmaceutical composition
 CC comprising the isolated anti-heparanase antibody or antibody portion and
 CC a pharmaceutical carrier. The antibody, methods, and composition are
 CC useful for detecting, treating, preventing or monitoring a pathological
 CC condition, e.g. angiogenesis, cell proliferation, a cancerous condition
 CC (blood, breast, bladder, rectum, stomach, cervix, ovarian, colon, renal,
 CC or prostate cancer), minor cell proliferation, invasion of circulating

CC tumour cells, or a metastatic disease, or a heparanase-related disorder
 CC or condition, e.g. an inflammatory disorder, wound, scar, vasculopathy
 CC (atherosclerosis, restenosis, or aneurysm), autoimmune condition, or
 CC renal disease or disorder (diabetic nephropathy, glomerulosclerosis,
 CC nephrotic syndrome, minimal change nephrotic syndrome, or a renal cell
 CC carcinoma) in a mammal. This sequence represents human heparanase.
 XX
 XX Sequence 543 AA;
 SQ
 Query Match 100.0%; Score 2841; DB 8; Length 543;
 Best Local Similarity 100.0%; Pred. No. 3e-275;
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLRSKPALPPPLMLLLGLPLSPGALPPAQAQVVDLDFQTEPLHLVSPSFLSVT 60
 DB 1 MLLRSKPALPPPLMLLLGLPLSPGALPPAQAQVVDLDFQTEPLHLVSPSFLSVT 60
 QY 61 IDANLATDPRFLILGLSPKLTARGLSPAYLRFGGTKTDFLIIDPKKSTFEERSYQWS 120
 DB 61 IDANLATDPRFLILGLSPKLTARGLSPAYLRFGGTKTDFLIIDPKKSTFEERSYQWS 120
 QY 121 QVNODICKYGSIPPDVEKLEWYQEQLLIREHYQKFKNSTYSRSSVDVLYTFANCS 180
 DB 121 QVNODICKYGSIPPDVEKLEWYQEQLLIREHYQKFKNSTYSRSSVDVLYTFANCS 180
 QY 181 GLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKADIFINGS 240
 DB 181 GLDLIFGLNALLRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKADIFINGS 240
 QY 241 QLGEDFTQLHKLKSTFKNAKLYGPDVGQPRRTAKMLKSLKAGGEVIDSVTWHHYVL 300
 DB 241 QLGEDFTQLHKLKSTFKNAKLYGPDVGQPRRTAKMLKSLKAGGEVIDSVTWHHYVL 300
 QY 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTPGKKVWLGETSSAYGGGAPLLSDTFA 360
 DB 301 NGRTATREDFLNPDVLDIFISSVQKVFQVVESTPGKKVWLGETSSAYGGGAPLLSDTFA 360
 QY 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNHLVDENFDPLDPYWLSSLFKKLVTGVLM 420
 DB 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNHLVDENFDPLDPYWLSSLFKKLVTGVLM 420
 QY 421 ASVQGSKRRLRVYLHCTNTDNPYKEDLTLAHLNHNVTYLRPLPYFFSNKQVDKYLL 480
 DB 421 ASVQGSKRRLRVYLHCTNTDNPYKEDLTLAHLNHNVTYLRPLPYFFSNKQVDKYLL 480
 QY 481 RPLGPHGLLSKSVQLNGITLKWVDDOTLPLMEKPLRPGSSIGLPAFSYSFFVIRNAKVA 540
 DB 481 RPLGPHGLLSKSVQLNGITLKWVDDOTLPLMEKPLRPGSSIGLPAFSYSFFVIRNAKVA 540
 QY 541 ACI 543
 DB 541 ACI 543
 RESULT 12
 ADY27036
 ID ADY27036 standard; protein; 543 AA.
 XX
 AC ADY27036;
 XX
 DT 05-MAY-2005 (first entry)
 XX
 DE Human heparanase protein.
 XX
 KW Heparanase; cancer; neoplasm; inflammation; cardiovascular disease;
 KW neurological disease; viral infection; infection; cytostatic;
 KW antiinflammatory; cardiovascular-gen.; neuroprotective; virucide;
 XX
 XX protease; enzyme; enzyme purification.
 OS
 XX Homo sapiens.
 XX
 XX WO2005016227-A2.
 XX

PD 24-FEB-2005.
XX 12-AUG-2004; 2004WO-IL000744.
XX 14-AUG-2003; 2003JUS-0494800P.
PR 12-JAN-2004; 2004US-0535492P.
XX (INSI-) INSIGHT BIOPHARMACEUTICALS LTD.
XX Van-Gelder JM, Miron D;
XX WPI; 2005-182203/19.
DR
XX
XX Regulating heparanase activity, useful for treating heparanase-associated
XX diseases (e.g. cancer, inflammation, cardiovascular diseases,
PT neurological diseases or viral diseases) comprises modulating heparanase
PT activation.
XX
XX Disclosure; SEQ ID NO 8; 211pp; English.
XX
XX The invention relates to a method of regulating heparanase activity in a
XX tissue or regulating a biological process depending at least in part on
CC heparanase activity comprising modulating heparanase activation. The
CC invention also relates to methods of treating a heparanase- or heparin
CC binding protein-associated disease or disorder in a subject, a
CC pharmaceutical composition for use in the treatment of a heparanase-
CC associated disease or disorder comprising a therapeutic amount of an
CC agent capable of modulating heparanase activation and a pharmaceutical
CC carrier or diluent, a method of identifying a protease activator of
CC heparanase, a protease substrate mimetic comprising a peptide
CC representing a subset or all substrate residues or cleavage sites of
CC human heparanase or an equivalent non-human heparanase, a method of
CC producing active heparanase and a method of modulating an adhesion
CC activity of heparanase. The composition and methods are useful for
CC modulating heparanase activation and for treating heparanase-associated
CC diseases or disorders such as cancer, inflammation, cardiovascular
CC diseases, neurological diseases or viral infections. This sequence
CC represents a human heparanase protein used in the scope of the invention.
XX
XX Sequence 543 AA;
SQ
Query Match 100.0%; Score 2841; DB 9; Length 543;
Best Local Similarity 100.0%; Pred. No. 3e-275;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLRSKPALPPPLMLLLGLPLSPGALPRPAQADVVLDLFFFTQEPHLVSPGFLSVT 60
DB 1 MLRSKPALPPPLMLLLGLPLSPGALPRPAQADVVLDLFFFTQEPHLVSPGFLSVT 60
QY 61 IDANLATDPRFLILGSPKLRTLARGLSPAYLRFGGTKTDFLIDPKKSTFEERSYMQS 120
DB 61 IDANLATDPRFLILGSPKLRTLARGLSPAYLRFGGTKTDFLIDPKKSTFEERSYMQS 120
QY 121 QVNQDICKYGSIPDPVEEKLREWPQEOQLLREHYQKFKNSTYSRSSVDVLYTFANC 180
DB 121 QVNQDICKYGSIPDPVEEKLREWPQEOQLLREHYQKFKNSTYSRSSVDVLYTFANC 180
QY 181 GLDLIFGLNALLRTADLWNSSNAQLLDYCSKGNISWELGNENPSFLKKADIFINGS 240
DB 181 GLDLIFGLNALLRTADLWNSSNAQLLDYCSKGNISWELGNENPSFLKKADIFINGS 240
QY 241 QLGEDFIQLHKLARKSTFKNAKLYGPDVGQPRKRTAKMLKSFLLKAGEVIDSVTHHYL 300
DB 241 QLGEDFIQLHKLARKSTFKNAKLYGPDVGQPRKRTAKMLKSFLLKAGEVIDSVTHHYL 300
QY 301 NGRTATREDPLNDVLDIFISSVQKVPQVVESTRPGKKVWLGETSSAYCGGAPLLSDTFA 360
DB 301 NGRTATREDPLNDVLDIFISSVQKVPQVVESTRPGKKVWLGETSSAYCGGAPLLSDTFA 360
QY 361 AGFMWLDKLGSLARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFVKLVGTVKVL 420
DB 361 AGFMWLDKLGSLARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSSLFVKLVGTVKVL 420

QY 421 ASVOGSKRRKRLRVYLHCTNTDNPYKGGDLTLVAINLHNVTKYLRLPSPNSKQVDKYLL 480
DB 421 ASVOGSKRRKRLRVYLHCTNTDNPYKGGDLTLVAINLHNVTKYLRLPSPNSKQVDKYLL 480
QY 481 RPLGPHGLLSKSVQLNGLTLLKMWDDQTLPLMEKPLRPGSLGLPAPFSYFFVIRNAKVA 540
DB 481 RPLGPHGLLSKSVQLNGLTLLKMWDDQTLPLMEKPLRPGSLGLPAPFSYFFVIRNAKVA 540
QY 541 ACI 543
DB 541 ACI 543
RESULT 13
AEA42426
ID AEA42426 standard; protein; 543 AA.
XX
XX AEA42426;
XX
XX 28-JUL-2005 (first entry)
XX Human heparanase protein SEQ ID NO:4.
XX antibody; heparanase; antiinflammatory; vulnerary; immunosuppressive;
KW antiangiogenic; cytostatic; antiarteriosclerotic; vasotropic;
KW inflammation; wound healing; scarring; vasculopathy; autoimmune disease;
KW angiogenesis disorder; cancer; tumor; metastasis.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 89..107
XX /note= "heparanase epitope SEQ ID NO:7"
XX Peptide 219..233
XX /note= "heparanase epitope SEQ ID NO:8"
XX Misc-difference 246
XX /note= "encoded by TAT"
XX Peptide 294..307
XX /note= "heparanase epitope SEQ ID NO:10"
XX Peptide 334..348
XX /note
XX Peptide 437..446
XX /note= "heparanase epitope SEQ ID NO:6"
XX AU2004201462-A1.
XX 06-MAY-2004.
XX 08-APR-2004; 2004AU-00201462.
XX 08-APR-2004; 2004AU-00201462.
XX (INSI-) INSIGHT BIOPHARMACEUTICALS LTD.
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
XX Vlodavsky I, Pecker I, Miron M, Gilboa A, Miron D, Moskowitz H;
PI Shlomi Y, Peleg Y, Yacoby-Zeevi O, Ayal-Hershkovitz M, Ben-Artzi H;
PI Feinstein E;
XX WPI; 2005-173343/19.
XX N-PSDB; AEA42434, AEA42435, AEA42460.
XX Novel isolated antibody capable of specifically binding to epitope of
XX heparanase protein, useful for preventing and treating heparanase-related
PT disorder such as inflammatory disorder, scars, autoimmune conditions or
PT angiogenesis.
XX Claim 2; SEQ ID NO 4; 260pp; English.
XX The invention relates to an isolated antibody or its portion (I) capable
CC of specifically binding to an epitope of a heparanase protein. Also
CC described: (1) a cell line (II) for producing a monoclonal antibody or
CC its portion, comprising a cell line for producing (I); (2) a

CC pharmaceutical composition comprising (I) and a carrier; and (3) an
CC affinity medium (III) for binding human heparanase polypeptides,
CC comprising (I) immobilized to a chemically inert, insoluble carrier. (I)
CC useful for treating a subject suffering from a pathological condition,
CC which involves administering (I) to the subject. (I) is useful for
CC preventing and treating heparanase-related disorder or condition chosen
CC from inflammatory disorder, wound, scar, vasculopathy, autoimmune
CC condition, angiogenesis, cell proliferation, cancerous condition, tumor
CC cell proliferation, invasion of circulating tumor cells and metastatic
CC disease. (I) is useful for detecting the presence of heparanase
CC polypeptide in a sample. (I) is useful for detecting heparanase-related
CC disease or condition in a subject such as vertebrate, preferably mammal
CC e.g., human. The heparanase-related disorder or condition further
CC includes renal disease or disorder chosen from diabetic nephropathy,
CC glomerulosclerosis, nephrotic syndrome, minimal change nephrotic syndrome
CC and renal cell carcinoma. The present sequence represents human
CC heparanase, which is used in the exemplification of the present
CC invention.

XX SQ Sequence 543 AA;

Query Match 100.0%; Score 2841; DB 9; Length 543;
Best Local Similarity 100.0%; Pred. No. 3e-275;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLRSKPALPPPLMLLLGLPLSPGALPRPAQADVVLDLFFFTQEPHLVSPSFLSVT 60
DB 1 MLLRSKPALPPPLMLLLGLPLSPGALPRPAQADVVLDLFFFTQEPHLVSPSFLSVT 60
QY 61 IDANLATDPRFLILGLSPKLTARGLSPAYLRFGTKTDFLI FDPKKESTFEERSYQWS 120
DB 61 IDANLATDPRFLILGLSPKLTARGLSPAYLRFGTKTDFLI FDPKKESTFEERSYQWS 120
QY 121 QVNQDICKYGSIPDPVEEKLRLWPYQOLLRLREHYQKKFNSTYSRSSVDVLYTFANCS 180
DB 121 QVNQDICKYGSIPDPVEEKLRLWPYQOLLRLREHYQKKFNSTYSRSSVDVLYTFANCS 180
QY 181 GLDLIFGLNALRTADLQWNSNAQLLDYCSKGYNISWELGNEPNSFLKKADIFINGS 240
DB 181 GLDLIFGLNALRTADLQWNSNAQLLDYCSKGYNISWELGNEPNSFLKKADIFINGS 240
QY 241 QLGEDFIQLHLLKRLSTFNKALYGPDVQGPQRRTAKMLKSPFKAGGEVIDSVTWHYYL 300
DB 241 QLGEDFIQLHLLKRLSTFNKALYGPDVQGPQRRTAKMLKSPFKAGGEVIDSVTWHYYL 300
QY 301 NGRATREDFLNPDLVDFISSVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 360
DB 301 NGRATREDFLNPDLVDFISSVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 360
QY 361 AGFMWLDKGLSARMGIEVVMQVFFGAGNYHLVDENFDPLPDYWLSSLFFKLVGTVKYL 420
DB 361 AGFMWLDKGLSARMGIEVVMQVFFGAGNYHLVDENFDPLPDYWLSSLFFKLVGTVKYL 420
QY 421 ASVQSGKRRKRLRVYLHCTNTDNPYKEGDLTIYALNHNVTYKLYRPFPSNKQVDKYL 480
DB 421 ASVQSGKRRKRLRVYLHCTNTDNPYKEGDLTIYALNHNVTYKLYRPFPSNKQVDKYL 480
QY 481 RPLGPHGLLSKSVQNLGLTKMVDQTLPLMEKPLRPGSSGLGLPAFYSFPIRNKVA 540
DB 481 RPLGPHGLLSKSVQNLGLTKMVDQTLPLMEKPLRPGSSGLGLPAFYSFPIRNKVA 540
QY 541 ACI 543
DB 541 ACI 543

RESULT 14

ID AAY30124
ID AAY30124 standard; protein; 588 AA.

XX
AC AAY30124;

XX
DT 20-MAR-2003 (revised)

DT 14-OCT-1999 (first entry)
XX A human protein with heparanase activity.
DE Human; heparanase; heparan sulfate; trauma; autoimmune disease;
XX skin disease; cardiovascular disease; nervous system disease;
KW Alzheimer's disease; cancer; cancer metastasis; angiogenesis;
KW inflammation; arthritis.
XX Homo sapiens.
XX WO9940207-A1.
PN 12-AUG-1999.
XX 05-FEB-1999; 99WO-EP000777.
PF 09-FEB-1999; 98GB-00002725.
PR (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA Nakajima M, Toyoshima M;
PI WPI; 1999-494300/41.
XX N-PSDB; AAX86671.
PT New heparanase polypeptide useful for treating autoimmune diseases, skin
PT diseases, cardiovascular diseases and nervous system diseases including
PT Alzheimer's disease.
PS Claim 3; Page 29-31; 40pp; English.
XX The present sequence represents a polypeptide with human heparanase
CC biological activity. Antagonists and inhibitors of the protein prevent it
CC from degrading the extracellular matrix and releasing heparan sulfate
CC from the extracellular matrix surface. The heparanase protein or the anti
CC -heparanase antibody are used in pharmaceutical compositions for treating
CC warm blooded animals suffering from a disease resulting from shortage or
CC lack of the heparanase protein, or from excessive activity or over-
CC expression of the heparanase protein, respectively. The heparanase
CC protein is used in treating diseases such as trauma, autoimmune disease,
CC skin diseases, cardiovascular diseases and nervous system diseases
CC including Alzheimer's disease resulting from shortage or lack of
CC polypeptide. The anti-heparanase antibody is used in treating the
CC diseases like cancer, cancer metastasis, angiogenesis and inflammation
CC including arthritis resulting from excessive activity or over expression
CC of heparanase protein. The anti-heparanase antibody can be used to detect
CC the presence or absence of polypeptide and its concentration. (Updated on
CC 20-MAR-2003 to correct PA field.)
XX SQ Sequence 588 AA;

Query Match 100.0%; Score 2841; DB 2; Length 588;
Best Local Similarity 100.0%; Pred. No. 3.5e-275;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLRSKPALPPPLMLLLGLPLSPGALPRPAQADVVLDLFFFTQEPHLVSPSFLSVT 60
DB 46 MLLRSKPALPPPLMLLLGLPLSPGALPRPAQADVVLDLFFFTQEPHLVSPSFLSVT 105
QY 61 IDANLATDPRFLILGLSPKLTARGLSPAYLRFGTKTDFLI FDPKKESTFEERSYQWS 120
DB 106 IDANLATDPRFLILGLSPKLTARGLSPAYLRFGTKTDFLI FDPKKESTFEERSYQWS 165
QY 121 QVNQDICKYGSIPDPVEEKLRLWPYQOLLRLREHYQKKFNSTYSRSSVDVLYTFANCS 180
DB 166 QVNQDICKYGSIPDPVEEKLRLWPYQOLLRLREHYQKKFNSTYSRSSVDVLYTFANCS 225
QY 181 GLDLIFGLNALRTADLQWNSNAQLLDYCSKGYNISWELGNEPNSFLKKADIFINGS 240
DB 226 GLDLIFGLNALRTADLQWNSNAQLLDYCSKGYNISWELGNEPNSFLKKADIFINGS 285

QY 241 OLGEDFIOLHKLRLKSTFKNAKLYGPDVQOPRRKTAKMLKSPFKAGGEVIDSVTWHYYL 300
DB 286 QLGEDFIOLHKLRLKSTFKNAKLYGPDVQOPRRKTAKMLKSPFKAGGEVIDSVTWHYYL 345
QY 301 NGRTATREDFLNPVDLIDIFISSVQKVFQVVESTRPCKKVLGETSSAYGGAPLLSDTFA 360
DB 346 NGRTATREDFLNPVDLIDIFISSVQKVFQVVESTRPCKKVLGETSSAYGGAPLLSDTFA 405
QY 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLDPYWLISLLFKLVGTQVLM 420
DB 406 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLDPYWLISLLFKLVGTQVLM 465
QY 421 ASVQSKRRKRLVYLHCTNTDNPYKEGDLTIYALNHNVTYLRPLPFPSNKQVDKYL 480
DB 466 ASVQSKRRKRLVYLHCTNTDNPYKEGDLTIYALNHNVTYLRPLPFPSNKQVDKYL 525
QY 481 RPLGPHGLLSKSVQLNGLTLKMWDDQTLPLPMEKPLRPGSSILGLPAFSYSFFVIRNAKVA 540
DB 526 RPLGPHGLLSKSVQLNGLTLKMWDDQTLPLPMEKPLRPGSSILGLPAFSYSFFVIRNAKVA 585
QY 541 ACI 543
DB 586 ACI 588

RESULT 15
AA02345
ID AA02345 standard; protein; 543 AA.
AC AA02345;
XX
DT 09-JUL-1999 (first entry)
XX
DE A human heparanase protein.
XX
KW Heparanase; hp; modulator; heparin-binding growth factor;
KW cellular response; cytokine; cell interaction; plasma lipoprotein;
KW cellular susceptibility; infection; disintegration;
KW neurodegenerative plaque; wound healing; angiogenesis; restenosis;
KW atherosclerosis; inflammation; neurodegenerative disease; neutralise;
KW plasma heparin; micrometastasis; autoimmune lesion; renal failure.
XX
OS Homo sapiens.
XX
PN WO9911798-A1.
XX
XX 11-MAR-1999.
XX 31-AUG-1998; 98WO-US017954.
XX 02-SEP-1997; 97US-00922170.
XX 02-JUL-1998; 98US-00109386.
XX
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA (FRIE/) FRIEDMAN M M.
XX
PI Pecker I, Vlodavsky I, Feinstein E;
XX
WPI; 1999-302255/25.
DR N-PSDB; AAX35648.
XX
XX New human polynucleotide useful for treating angiogenesis, restenosis,
PT and inflammation.
XX
XX Claim 6; Fig 1; 63pp; English.

XX The specification describes a polypeptide having heparanase (hp)
CC activity. The recombinant protein is used as a modulator of heparin-
CC binding growth factors, cellular responses to heparin-binding growth
CC factors and cytokines, cell interaction with plasma lipoproteins,
CC cellular susceptibility to viral, protozoal and bacterial infections or
CC disintegration of neurodegenerative plaques. Heparanase may be useful for

CC conditions such as wound healing, angiogenesis, restenosis,
CC atherosclerosis, inflammation, neurodegenerative diseases, and viral
CC infections. Mammalian heparanase can be used to neutralize plasma
CC heparin, and anti-heparanase antibodies may be applied for
CC immunodetection and diagnosis of micrometastases, autoimmune lesions, and
CC renal failure in biopsy specimens, plasma samples, and body fluids. The
CC present sequence represents human heparanase
XX
SQ Sequence 543 AA;

Query Match 99.9%; Score 2838; DB 2; Length 543;
Best Local Similarity 99.8%; Pred. No. 6.1e-275;
Matches 542; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLSKPALPPLMLLLGPIGPIGSPGALPRPAQADVVLDLDFFTQEPHLHLVSPFLSVT 60
DB 1 MLLSKPALPPLMLLLGPIGPIGSPGALPRPAQADVVLDLDFFTQEPHLHLVSPFLSVT 60
QY 61 IDANLATDPRFLILIGSPKRLTLARGLSPAYLRFGGTKTDFLIDFPKKESTPEERSYMQS 120
DB 61 IDANLATDPRFLILIGSPKRLTLARGLSPAYLRFGGTKTDFLIDFPKKESTPEERSYMQS 120
QY 121 QVNQDICKYGSIPDPVEEKLRLWPYQBLRLREHYQKFKNSTYSRSVDVLYTFANCS 180
DB 121 QVNQDICKYGSIPDPVEEKLRLWPYQBLRLREHYQKFKNSTYSRSVDVLYTFANCS 180
QY 181 GLDLIFGLNALLRTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
DB 181 GLDLIFGLNALLRTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
QY 241 OLGEDFIOLHKLRLKSTFKNAKLYGPDVQOPRRKTAKMLKSPFKAGGEVIDSVTWHYYL 300
DB 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVQOPRRKTAKMLKSPFKAGGEVIDSVTWHYYL 300
QY 301 NGRTATREDFLNPVDLIDIFISSVQKVFQVVESTRPCKKVLGETSSAYGGAPLLSDTFA 360
DB 301 NGRTATREDFLNPVDLIDIFISSVQKVFQVVESTRPCKKVLGETSSAYGGAPLLSDTFA 360
QY 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLDPYWLISLLFKLVGTQVLM 420
DB 361 AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLDPYWLISLLFKLVGTQVLM 420
QY 421 ASVQSKRRKRLVYLHCTNTDNPYKEGDLTIYALNHNVTYLRPLPFPSNKQVDKYL 480
DB 421 ASVQSKRRKRLVYLHCTNTDNPYKEGDLTIYALNHNVTYLRPLPFPSNKQVDKYL 480
QY 481 RPLGPHGLLSKSVQLNGLTLKMWDDQTLPLPMEKPLRPGSSILGLPAFSYSFFVIRNAKVA 540
DB 481 RPLGPHGLLSKSVQLNGLTLKMWDDQTLPLPMEKPLRPGSSILGLPAFSYSFFVIRNAKVA 540
QY 541 ACI 543
DB 541 ACI 543

Search completed: February 27, 2006, 17:46:54
Job time : 190 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 04:40:00 ; Search time 1068 Seconds
(without alignments)
10739.640 Million cell updates/sec

Title: SEQ1-799T
Perfect score: 1721
Sequence: 1 ctgagagtttcgactctcg.....atatactagtcctgacactg 1721

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : N_Geneseq_21.*
- 1: Geneseqn1980s.*
 - 2: Geneseqn1990s.*
 - 3: Geneseqn2000s.*
 - 4: Geneseqn2001as.*
 - 5: Geneseqn2001bs.*
 - 6: Geneseqn2002as.*
 - 7: Geneseqn2002bs.*
 - 8: Geneseqn2003as.*
 - 9: Geneseqn2003bs.*
 - 10: Geneseqn2003cs.*
 - 11: Geneseqn2003ds.*
 - 12: Geneseqn2004as.*
 - 13: Geneseqn2004bs.*
 - 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1719.4	99.9	1721	2	AAX35648
2	1719.4	99.9	1721	3	AAX39195
3	1719.4	99.9	1721	3	AA75051
4	1719.4	99.9	1721	3	AAX33290
5	1719.4	99.9	1721	4	AA91112
6	1719.4	99.9	1721	10	ADG8801
7	1719.4	99.9	1721	10	ADG88799
8	1719.4	99.9	1721	12	ADL16380
9	1719.4	99.9	1721	12	ADL16378
10	1719.4	99.9	1721	12	ADM48717
11	1719.4	99.9	1721	12	ADM48715
12	1719.4	99.9	1721	14	AEA42434
13	1719.4	99.9	1721	14	AEA42435
14	1717.8	99.8	1899	2	AAX35650
15	1717.8	99.8	1899	3	AA75053
16	1717.8	99.8	1899	10	ADG8803
17	1717.8	99.8	1899	10	ADG88805
18	1717.8	99.8	1899	12	ADL16384
19	1717.8	99.8	1899	12	ADL16382

20	1717.8	99.8	1899	12	ADM48719
21	1717.8	99.8	1899	12	ADM48721
22	1717.8	99.8	1899	14	AEA42460
23	1714.6	99.6	1722	5	AAF93788
24	1714.6	99.6	1722	14	ADY63086
25	1699.4	98.7	1701	14	AEA42485
26	1696.2	98.6	1713	2	AAX37259
27	1690.4	98.2	1723	2	AAX37260
28	1688.4	98.1	3726	2	AAX86671
29	1688.4	98.1	3726	10	AD18951
30	1688.4	98.1	3726	12	ADK51968
31	1688.4	98.1	3726	12	ADN04901
32	1688.4	98.1	3726	12	ADN05073
33	1688.4	98.1	3726	13	ADP25078
34	1688.4	98.1	3726	13	ADP25078
35	1684.2	97.9	1724	4	AAH20940
36	1649.6	95.9	1673	12	ADO63816
37	1649.6	95.9	1673	12	ADO63817
38	1648	95.8	1673	12	ADO63818
39	1633	94.9	1669	8	ABZ22816
40	1633	94.9	1669	10	ADL16011
41	1631.4	94.8	1669	12	ADL193950
42	1586.6	92.2	1593	2	AAZ11236
43	1578.4	91.7	1668	14	AD219009
44	1555.8	90.4	1625	12	ADO63819
45	1555.8	90.4	1625	12	ADO63820

ALIGNMENTS

RESULT 1

AAX35648
ID AAX35648 standard; cDNA; 1721 BP.
XX
AC AAX35648;
XX
DT 09-JUL-1999 (first entry)
XX
DE cDNA encoding a human heparanase protein.
XX
KW Heparanase; hpa; modulator; heparin-binding growth factor;
KW cellular response; cytokine; cell interaction; plasma lipoprotein;
KW cellular susceptibility; infection; disintegration;
KW neurodegenerative plaque; wound healing; angiogenesis; restenosis;
KW atherosclerosis; inflammation; neurodegenerative disease; neutralise;
KW plasma heparin; micrometastasis; autoimmune lesion; renal failure; ss.
XX Homo sapiens.
XX
XX WO9911798-A1.
XX
XX PD 11-MAR-1999.
XX
XX PF 31-AUG-1998; 98WO-US017954.
XX
XX PR 02-SEP-1997; 97US-00922170.
XX
XX PR 02-JUL-1997; 98US-00109386.
XX
XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX (FRIE/) FRIEDMAN M M.
XX
XX PI Pecker I, Vlodavsky I, Feinstein B;
XX
XX DR WPI; 1999-302255/25.
XX
XX DR P-PSDB; AAY02345.
XX
XX PT New human polynucleotide useful for treating angiogenesis, restenosis,
XX and inflammation.
XX
XX PS Claim 4; Fig 1; 63pp; English.
XX

CC The specification describes a polypeptide having heparanase (hpa)
CC activity. The recombinant protein is used as a modulator of heparin-
CC binding growth factors, cellular responses to heparin-binding growth
CC factors and cytokines, cell interaction with plasma lipoproteins,
CC cellular susceptibility to viral, protozoal and bacterial infections or
CC disintegration of neurodegenerative plaques. Heparanase may be useful for
CC conditions such as wound healing, angiogenesis, restenosis,
CC atherosclerosis, inflammation, neurodegenerative diseases, and viral
CC infections. Mammalian heparanase can be used to neutralize plasma
CC heparin, and anti-heparanase antibodies may be applied for
CC immunodetection and diagnosis of micrometastases, autoimmune lesions, and
CC renal failure in biopsy specimens, plasma samples, and body fluids. The
CC present sequence encodes human heparanase
XX
XX

Seq 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match		99.9%; Score 1719.4; DB 2; Length 1721;
Best Local Similarity		99.9%; Pred. No. 0;
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
Qy	1	CTAGAGCTTTGCACTCCGCTGCGCGCAGCTGGCGGGGAGCAGCCAGGTGAGCCCA 60
Db	1	CTAGAGCTTTGCACTCCGCTGCGCGCAGCTGGCGGGGAGCAGCCAGGTGAGCCCA 60
Qy	61	AGATGCTGCTGCGCTCGAAGCCTGCGCTGCCCGCCGCTGATGCTGCTCTGGGGC 120
Db	61	AGATGCTGCTGCGCTCGAAGCCTGCGCTGCCCGCCGCTGATGCTGCTCTGGGGC 120
Qy	121	CGCTGGGTCCCTCTCCCTGCGCGCCCTGCGCCGCTGATGCTGCTCTGGGGC 180
Db	121	CGCTGGGTCCCTCTCCCTGCGCGCCCTGCGCCGCTGATGCTGCTCTGGGGC 180
Qy	181	ACCTGGACTCTTCAACCCAGAGCGCTGACCTGCTGGAGCCCTCTCTGCTGCTCA 240
Db	181	ACCTGGACTCTTCAACCCAGAGCGCTGACCTGCTGGAGCCCTCTCTGCTGCTCA 240
Qy	241	CCATTGACGCCAACTGGCCACGACCGCGGTTCCTCATCTCTCGGTTCCTCAAGC 300
Db	241	CCATTGACGCCAACTGGCCACGACCGCGGTTCCTCATCTCTCGGTTCCTCAAGC 300
Qy	301	TTCTGACTCTGGCCAGAGGCTTGCTCTCTGCTGCTACCTGAGTTTGGTGGCAAGACAG 360
Db	301	TTCTGACTCTGGCCAGAGGCTTGCTCTCTGCTGCTACCTGAGTTTGGTGGCAAGACAG 360
Qy	361	ACTTCCTAAATTTTCATCCCAAGAGGAATCAACCTTTGAGAGAGAAATTTACTGGCAAT 420
Db	361	ACTTCCTAAATTTTCATCCCAAGAGGAATCAACCTTTGAGAGAGAAATTTACTGGCAAT 420
Qy	421	CTCAAGTCAACAGAGATTTGCAAAATATGATCCATCCCTCTCTGATGTGGAGAGAGT 480
Db	421	CTCAAGTCAACAGAGATTTGCAAAATATGATCCATCCCTCTCTGATGTGGAGAGAGT 480
Qy	481	TACGGTTGGAAATGGCCCTACAGGAGCAATTTGCTACTCCGAGAACACTACACAGAAAAGT 540
Db	481	TACGGTTGGAAATGGCCCTACAGGAGCAATTTGCTACTCCGAGAACACTACACAGAAAAGT 540
Qy	541	TCAAGACAGACACCTACTCAAGAGAGCTGTAGATGTGCTATACACTTTTGCAAACTGCT 600
Db	541	TCAAGACAGACACCTACTCAAGAGAGCTGTAGATGTGCTATACACTTTTGCAAACTGCT 600
Qy	601	CAGGACTGGACTGTGATCTTTGGCTTAAATGGTTATTAAAGAACAGCAGATTTGAGTGGGA 660
Db	601	CAGGACTGGACTGTGATCTTTGGCTTAAATGGTTATTAAAGAACAGCAGATTTGAGTGGGA 660
Qy	661	ACAGTTCTAAATGCTCAGTTGCTCTGGACTACTGCTCTTCCAGGGGTATAACATTTCTT 720
Db	661	ACAGTTCTAAATGCTCAGTTGCTCTGGACTACTGCTCTTCCAGGGGTATAACATTTCTT 720
Qy	721	GGGAACAGGCAATGAACCTAACAGTTTCTTAAAGAGGCTGATATTTTCATCAATGGGT 780
Db	721	GGGAACAGGCAATGAACCTAACAGTTTCTTAAAGAGGCTGATATTTTCATCAATGGGT 780
Qy	781	CGCAGTTAGGAGAGATTTTATTCATTTGATATAAACTTCTTAAGAAAGTCCACCTTCAAAA 840

Db	781	CGCAGTTAGGAGAGATTTATATTAATTCATTAATAACTTCTCAAGAAAGTCCACCTTCAAAA 840
Qy	841	ATGCAAAACTCTATGCTCTGATGTTGGTCCAGCTCGAAGAAAGACGGCTAAGATGCTGA 900
Db	841	ATGCAAAACTCTATGCTCTGATGTTGGTCCAGCTCGAAGAAAGACGGCTAAGATGCTGA 900
Qy	901	AGAGCTTCCCTGAAGGCTGGTGGAGAGATGATTCATTACATTCAGTTACATGCATCTACTATT 960
Db	901	AGAGCTTCCCTGAAGGCTGGTGGAGAGATGATTCATTACATTCAGTTACATGCATCTACTATT 960
Qy	961	TGAATGGACGCACTGCTACCCAGGGAAGATTTCTTAAACCTCTGATTTAGCAATTTTTA 1020
Db	961	TGAATGGACGCACTGCTACCCAGGGAAGATTTCTTAAACCTCTGATTTAGCAATTTTTA 1020
Qy	1021	TTTCACTGTGCAAAAAGTTTTTCCAGGTGGTGGAGCAGCCCTGGCAAGAGTCT 1080
Db	1021	TTTCACTGTGCAAAAAGTTTTTCCAGGTGGTGGAGCAGCCCTGGCAAGAGTCT 1080
Qy	1081	GGTTAGGAGAAACAAGCTCTGCAATATGGAGCGGAGCGCCCTTGCTATCCGACACCTTTG 1140
Db	1081	GGTTAGGAGAAACAAGCTCTGCAATATGGAGCGGAGCGCCCTTGCTATCCGACACCTTTG 1140
Qy	1141	CAGCTGGCTTTATGCTGGCTGGAATAAATTTGGGCCCTGTGAGCCCGAATGGGAATAGAAGTG 1200
Db	1141	CAGCTGGCTTTATGCTGGCTGGAATAAATTTGGGCCCTGTGAGCCCGAATGGGAATAGAAGTG 1200
Qy	1201	TGATGAGGCAAGTATTTCTTTGGAGCAGGAAACCTACCATTTAGTGGATGAAACCTTCGATC 1260
Db	1201	TGATGAGGCAAGTATTTCTTTGGAGCAGGAAACCTACCATTTAGTGGATGAAACCTTCGATC 1260
Qy	1261	CTTTACCTGATTTATGCTGCTATCTCTCTGTTCAAGAAATTTGGTGGCACCAGGTGTAA 1320
Db	1261	CTTTACCTGATTTATGCTGCTATCTCTCTGTTCAAGAAATTTGGTGGCACCAGGTGTAA 1320
Qy	1321	TGGCAAGCGTCAAGGTTCAAAGAGAGGAAGCTTCGAGTATACCTTCATTGCACAAAACA 1380
Db	1321	TGGCAAGCGTCAAGGTTCAAAGAGAGGAAGCTTCGAGTATACCTTCATTGCACAAAACA 1380
Qy	1381	CTGACAAATCAAGGTATAAAGAGGAGATTTAACTCTGATGCAATAAACCTCCATAACG 1440
Db	1381	CTGACAAATCAAGGTATAAAGAGGAGATTTAACTCTGATGCAATAAACCTCCATAACG 1440
Qy	1441	TCACCAAGTACTTGGCGTTACCTATCCCTTTTCTAACCAAGCAAGTGGATAAATACCTTC 1500
Db	1441	TCACCAAGTACTTGGCGTTACCTATCCCTTTTCTAACCAAGCAAGTGGATAAATACCTTC 1500
Qy	1501	TAAGACCTTTGGGACCTCATGGATTTACTTTCCAAAATCTGTCCAACTCAATGGTCTAACTC 1560
Db	1501	TAAGACCTTTGGGACCTCATGGATTTACTTTCCAAAATCTGTCCAACTCAATGGTCTAACTC 1560
Qy	1561	TAAAGATGGTGGATGATCAAAACCTTGGCACCTTTAAATGGAAAAACCTCTCCGGCAGGAA 1620
Db	1561	TAAAGATGGTGGATGATCAAAACCTTGGCACCTTTAAATGGAAAAACCTCTCCGGCAGGAA 1620
Qy	1621	GTTCACTGGCTTGGCAGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680
Db	1621	GTTCACTGGCTTGGCAGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680
Qy	1681	CTGCTTGCATCTGAAAATAAAATATATCTAGTCTCTGCACCTG 1721
Db	1681	CTGCTTGCATCTGAAAATAAAATATATCTAGTCTCTGCACCTG 1721

RESULT 2

AAZ39195

ID AAZ39195 standard; cdna; 1721 BP.

XX AAZ39195;

AC AAZ39195;

XX 02-MAR-2000 (first entry)

XX Human heparanase encoding cdna.

DE

XX Human; heparanase; hpa; genetic modification; expression; anticancer; angiogenesis; anti-angiogenic; antiproliferative; antiviral; antitumour; KW anti-atherosclerotic; anti-inflammatory; antineurodegeneration; KW heparan sulphate; heparin-binding growth factor; tumour angiogenesis; KW metastasis; wound healing; restenosis; atherosclerosis; inflammation; KW neurodegeneration; viral infection; cystic fibrosis; cancer; diagnosis; KW micrometastasis; autoimmune lesion; kidney failure; ss.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT CDS 63..1694

FT /*tag= a

FT /product= "heparanase"

XX WO957244-A1.

XX 11-NOV-1999.

XX 29-APR-1999; 99WO-US009256.

XX 01-MAY-1998; 98US-00071618.

XX 02-MAR-1999; 99US-00260038.

XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.

XX (FRIE/) FRIEDMAN M M.

XX Ben-Artzi H, Ayal-Hershkovitz M, Yacoby-Zeevi O, Pecker I;

XX Peleg Y, Shlomi Y;

XX WP1; 2000-062144/05.

XX P-PSDB; AAY57590.

XX Engineered cells that express recombinant heparanase, useful

PT therapeutically, e.g. for treating angiogenesis and to screen for

PT specific inhibitors, potential anticancer agents.

XX Claim 2; Page 106-107; 118pp; English.

XX The present invention describes genetically modified cells (A) containing

CC a polynucleotide (I) that encodes a polypeptide with heparanase activity,

CC and express recombinant heparanase (II). Heparanase cleaves heparan

CC sulphate (HS) at specific intrachain sites, resulting in release of

CC heparin-binding growth factors, enzymes and proteins that are sequestered

CC by HS in basement membranes, extracellular matrix or cell surfaces. It

CC may also be implicated in tumour angiogenesis and metastases. (II) is

CC potentially useful in wound healing and for treating angiogenesis,

CC restenosis, atherosclerosis, inflammation, neurodegeneration, viral

CC infection and cystic fibrosis. It can also be used to neutralise heparin

CC (an alternative to protamine) and to screen for specific inhibitors

CC (potentially useful for treating cancer and metastases). Antibodies

CC raised against (II) are used for immunodetection and diagnosis of

CC micrometastases, autoimmune lesions and kidney failure. (A) provide (II)

CC in large quantities, in a form that is homogeneously processed and

CC activated/neutralised by a dedicated protease. The present sequence

CC encodes human heparanase

XX Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

XX

Query Match 99.9%; Score 1719.4; DB 3; Length 1721;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTAGAGCTTTGCACTCTCCGCTGGCGGAGCTGGCGGGGGAGCAGCCAGGTGAGCCCA 60

DB 1 CTAGAGCTTTGCACTCTCCGCTGGCGGAGCTGGCGGGGGAGCAGCCAGGTGAGCCCA 60

QY 61 AGATGCTGCTGCGCTCGAAGCCTGCGCTGGCGCGCGCTGATGCTGCTCTCTGGGGC 120

DB 61 AGATGCTGCTGCGCTCGAAGCCTGCGCTGGCGCGCGCTGATGCTGCTCTCTGGGGC 120

QY 121 CGCTGGGTCCCTCTCCCTTGGCGCCCTGCCCCGACCTGCGCAAGCAGCAGCGTGTGG 180

121 CGCTGGGTCCCTCTCCCTTGGCGCCCTGCCCCGACCTGCGCAAGCAGCAGCGTGTGG 180

181 ACCTGCACTTCTTCAACCAGGAGCGCTGCACCTGGTGAGCCCTCTGTTCTCTGTCCTCA 240

181 ACCTGCACTTCTTCAACCAGGAGCGCTGCACCTGGTGAGCCCTCTGTTCTCTGTCCTCA 240

241 CCAATTGACGCAACCTGGCCACGAGCCGCGGTCTCTCATCTCTCTCTCTCTCTCTCTCT 300

241 CCAATTGACGCAACCTGGCCACGAGCCGCGGTCTCTCATCTCTCTCTCTCTCTCTCTCT 300

301 TTGCTACCTTGGCCAGAGGCTTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

301 TTGCTACCTTGGCCAGAGGCTTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

361 ACTTCTCTTAATTTTCGATCCCAAGAAGAAATCAACCTTTGAAGAGAGAAATTTACTTGG 420

361 ACTTCTCTTAATTTTCGATCCCAAGAAGAAATCAACCTTTGAAGAGAGAAATTTACTTGG 420

421 CTCAAGTCAACACAGGATATTTGCAATATGATTCATCTCTCTCTCTCTCTCTCTCTCTCT 480

421 CTCAAGTCAACACAGGATATTTGCAATATGATTCATCTCTCTCTCTCTCTCTCTCTCTCT 480

481 TAGCGTTGGAATGGCCCTTACAGGAGCAATTTGCTACTCCGAGAACACTTACAGAAAAGT 540

481 TAGCGTTGGAATGGCCCTTACAGGAGCAATTTGCTACTCCGAGAACACTTACAGAAAAGT 540

541 TCAAGAACAGCACTACTCTCAAGAAGCTCTGTAGATGTGTATACATCTTTTGGCAAACTG 600

541 TCAAGAACAGCACTACTCTCAAGAAGCTCTGTAGATGTGTATACATCTTTTGGCAAACTG 600

601 CAGGACTGGACTTTGATCTTTTGGCTAAATCGTTATTAAGAACAGCAGATTTTGCAGTGG 660

601 CAGGACTGGACTTTGATCTTTTGGCTAAATCGTTATTAAGAACAGCAGATTTTGCAGTGG 660

661 ACAGTTCTAATGCTCAGTTGCTCTCTGCACTACTGCTCTTCCAGAGGGGTATAACATTTCT 720

661 ACAGTTCTAATGCTCAGTTGCTCTCTGCACTACTGCTCTTCCAGAGGGGTATAACATTTCT 720

721 GGGAACTAGGCAATGAACCTTAACAGTTTCTTAAAGAGGCTGATATTTTTCATCAATGGGT 780

721 GGGAACTAGGCAATGAACCTTAACAGTTTCTTAAAGAGGCTGATATTTTTCATCAATGGGT 780

781 CGCAGTTAGGAGAAAGATTTTATTTCAATTCATATAAATTTCTTAAGAAAAGTCCACCTT 840

781 CGCAGTTAGGAGAAAGATTTTATTTCAATTCATATAAATTTCTTAAGAAAAGTCCACCTT 840

841 ATGCAAAACTCTATGCTCTGATGTTGGTTCAGCTCGAAGAAAGACGGCTAAGATGCTGA 900

841 ATGCAAAACTCTATGCTCTGATGTTGGTTCAGCTCGAAGAAAGACGGCTAAGATGCTGA 900

901 AGAGCTTCTGAGGCTGGTGGAGAGTGAATTCAGTTACATGSCATCCTACTACTATT 960

901 AGAGCTTCTGAGGCTGGTGGAGAGTGAATTCAGTTACATGSCATCCTACTACTATT 960

961 TGAATGGAGCGGACTGCTACAGGGAAGATTTTCTAAACCTCTGATGTTATGGACATTTT 1020

961 TGAATGGAGCGGACTGCTACAGGGAAGATTTTCTAAACCTCTGATGTTATGGACATTTT 1020

1021 TTTTCATCTGTGCAAAAAGTTTCCAGGTGTTGAGAGCACAGGCTTGGCAAGAGGTCT 1080

1021 TTTTCATCTGTGCAAAAAGTTTCCAGGTGTTGAGAGCACAGGCTTGGCAAGAGGTCT 1080

1081 GGTTAGGAGAAACAAGCTCTGCATATGGAGGGGGGGCCCTTGTCTATCCGACACCTTTG 1140

1081 GGTTAGGAGAAACAAGCTCTGCATATGGAGGGGGGGCCCTTGTCTATCCGACACCTTTG 1140

1141 CAGCTGGCTTTATGTCGCTGGATAAATTTGGCCCTGTGAGCCGGAATGGGAATAGAAGTGG 1200

1141 CAGCTGGCTTTATGTCGCTGGATAAATTTGGCCCTGTGAGCCGGAATGGGAATAGAAGTGG 1200

1201 TGATGAGGAAGTATTTCTTTTGGAGCAGGAAATTAACATTTAGTGGATGAAAACCTTCGATC 1260

Db	1201	1201	TGATGAGCGCAAGTATTCTTTGGAGCAGGAACCTACCAATTTAGTGGATGAAACCTTCGATC	1260
Qy	1261	1261	CTTTACCTGATATTATGGCTATCTCTCTGTTCAAGAAATTTGGTGGGCACCAAGGTGTAA	1320
Db	1261	1261	CTTTACCTGATATTATGGCTATCTCTCTGTTCAAGAAATTTGGTGGGCACCAAGGTGTAA	1320
Qy	1321	1321	TGGCAAGGGTGCAGGTTTCAAGAGAGAGGAGCTTTCGAGTATACCTTCATTGCAACAACA	1380
Db	1321	1321	TGGCAAGGGTGCAGGTTTCAAGAGAGAGGAGCTTTCGAGTATACCTTCATTGCAACAACA	1380
Qy	1381	1381	CTGCACATCCAAAGGTATAAAGAGGAGATTTAACTCTGTATGCCATAAACTCCATAAAG	1440
Db	1381	1381	CTGCACATCCAAAGGTATAAAGAGGAGATTTAACTCTGTATGCCATAAACTCCATAAAG	1440
Qy	1441	1441	TCACCAAGTACTTGGCGTTACCCCTATCCTTTTCTTAACAAGCAGAGTGGATAATACCTTC	1500
Db	1441	1441	TCACCAAGTACTTGGCGTTACCCCTATCCTTTTCTTAACAAGCAGAGTGGATAATACCTTC	1500
Qy	1501	1501	TAAGACCTTTGGGACCTCATGGATTACTTTCCAAATCTGCCAACTCAATGGGTCTAACTC	1560
Db	1501	1501	TAAGACCTTTGGGACCTCATGGATTACTTTCCAAATCTGTCCAACTCAATGGGTCTAACTC	1560
Qy	1561	1561	TAAAGATGGTGGATGATCAAAACCTTGCCACCTTTTAATGGAAAAACCTCTCCGGCCAGGAA	1620
Db	1561	1561	TAAAGATGGTGGATGATCAAAACCTTGCCACCTTTTAATGGAAAAACCTCTCCGGCCAGGAA	1620
Qy	1621	1621	GTTCACTGGGCTGCCAGCTTTCATATAGTTTTTTTTTGTATGAAGAAATGCCAAAGTTG	1680
Db	1621	1621	GTTCACTGGGCTGCCAGCTTTCATATAGTTTTTTTTTGTATGAAGAAATGCCAAAGTTG	1680
Qy	1681	1681	CTGCTTGCATCTGAAAAATAAATAATACTAGTCTCGACACTG	1721
Db	1681	1681	CTGCTTGCATCTGAAAAATAAATAATACTAGTCTCGACACTG	1721

RESULT 3

AAA75051
ID AAA75051 standard: CDNA: 1721 BP.

XX
AC AAA75051:XX
DT 15-JAN-2001 (first entry)

XX DE CDNA encoding a human heparanase polypeptide.

XX Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
KW heparin-binding growth factor; cytokine; neurodegenerative plaque;
KW wound healing; infection; burn; angiogenesis; restenosis;
KW atherosclerosis; inflammation; neurodegenerative disease;
KW Gerstmann-Sträussler Syndrome; Creutzfeldt-Jakob disease; ds.

XX
OS Homo sapiens.

XX	Key	Location/Qualifiers
PH	CDS	63..1693
FT		/tag= a
FT		/product= "heparanase"
FT	stem loop	698..724

XX PN WO200052178-A1.

XX PD 08-SEP-2000.

14-FEB-2000: 2000WO-US003542.

XX
PR 01-MAR-1999: 99US-00258892.

XX (PA) (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA (FRIE/) FRIEDMAN M M.

Qy	601	CAGGACTGGGACTTGCATCTTTGGCCATAATCGGTTATTTAAGAA	CAGCAGAGATTTGCAGTGGG	660	
Db	601	CAGGACTGGGACTTGCATCTTTGGCCATAATCGGTTATTTAAGAA	CAGCAGAGATTTGCAGTGGG	660	
Qy	661	ACAGTTCTAATGCTCAGTGTGCTCCTCGACTACTGCTCTTC	CAAGGGGCTATAACAATTTCTT	720	
Db	661	ACAGTTCTAATGCTCAGTGTGCTCCTCGACTACTGCTCTTC	CAAGGGGCTATAACAATTTCTT	720	
Qy	721	GGGAACTAGGCAATAGAA	CCTAACAAGTTTCCTTAAGAAAGGCTGATATTTT	CATCAATGGGT	780
Db	721	GGGAACTAGGCAATAGAA	CCTAACAAGTTTCCTTAAGAAAGGCTGATATTTT	CATCAATGGGT	780
Qy	781	CGCAGTTAGGAGAAGATTTTATTCAA	TGCGATATAAACCCTTAAGAAAGCTCACCTTCAAAA	840	
Db	781	CGCAGTTAGGAGAAGATTTATTCAA	TGCGATATAAACCCTTAAGAAAGCTCACCTTCAAAA	840	
Qy	841	ATGCAAAATCTATGGTCTCTGATGTGGT	CAGCCTCGAAGAAAGACGGCTAAGATGCTGA	900	
Db	841	ATGCAAAATCTATGGTCTCTGATGTGGT	CAGCCTCGAAGAAAGACGGCTAAGATGCTGA	900	
Qy	901	AGAGCTTCTGAAAGGCTGGTGGAGAAGTGATTGATT	CAGTTACATGCGCATCTACTTACTT	960	
Db	901	AGAGCTTCTGAAAGGCTGGTGGAGAAGTGATTGATT	CAGTTACATGCGCATCTACTTACTT	960	
Qy	961	TGAATGSCACGGACTGCTACACAGGGAAGATTTTCTAA	ACCCCTGATGTATTTGGACATTTTTTA	1020	
Db	961	TGAATGSCACGGACTGCTACACAGGGAAGATTTTCTAA	ACCCCTGATGTATTTGGACATTTTTTA	1020	
Qy	1021	TTTTCATCTGTGCAAAAAGTTTTCCAGGTGGTGTGAGAC	CACAGGCCCTGGCAAGAAGTCT	1080	
Db	1021	TTTTCATCTGTGCAAAAAGTTTTCCAGGTGGTGTGAGAC	CACAGGCCCTGGCAAGAAGTCT	1080	
Qy	1081	GGTTAGGAGAAA	CAAGCTCTGCATATGGAGCGCGAGCGCCCTTGCTAT	CGGACACCTTTG	1140
Db	1081	GGTTAGGAGAAA	CAAGCTCTGCATATGGAGCGCGAGCGCCCTTGCTAT	CGGACACCTTTG	1140
Qy	1141	CAGCTGGCTTTATGTGCTCGATAAATTTGGGCTGT	CAGCCGAATGGGAATAGAAGTGG	1200	
Db	1141	CAGCTGGCTTTATGTGCTCGATAAATTTGGGCTGT	CAGCCGAATGGGAATAGAAGTGG	1200	
Qy	1201	TGATGGGCAAGTATTTCTTTGGAGCAGGAAC	TACCAATTTAGTGGATGAAGAACTTCGATC	1260	
Db	1201	TGATGGGCAAGTATTTCTTTGGAGCAGGAAC	TACCAATTTAGTGGATGAAGAACTTCGATC	1260	
Qy	1261	CTTTTACCTGATATTTGGCTATCTCTTCTGTT	CAAGAAATTTGGTGGGCA	CCAAAGTGTTAA	1320
Db	1261	CTTTTACCTGATATTTGGCTATCTCTTCTGTT	CAAGAAATTTGGTGGGCA	CCAAAGTGTTAA	1320
Qy	1321	TGGCAAGCTGCAAGGTTTCAAAGAGAGAGGAGCTT	CGAGTATACCTTTCANTGCA	CAAAACA	1380
Db	1321	TGGCAAGCTGCAAGGTTTCAAAGAGAGAGGAGCTT	CGAGTATACCTTTCANTGCA	CAAAACA	1380
Qy	1381	CTGCACATCCAAAGTATAAAGAGGAGATTTAACT	CTGTATGCCATAAACCCTCCATAACG	1440	
Db	1381	CTGCACATCCAAAGTATAAAGAGGAGATTTAACT	CTGTATGCCATAAACCCTCCATAACG	1440	
Qy	1441	TCACCAAGTACTTGGCGGTTACCCCTATCCTTTTCT	TAAACAAGTGGGATAAATACCTTC	1500	
Db	1441	TCACCAAGTACTTGGCGGTTACCCCTATCCTTTTCT	TAAACAAGTGGGATAAATACCTTC	1500	
Qy	1501	TAAAGCCTTTGGGACCTCATGGATTA	CTTTCCAAATCTGTCCAACTCAATGGTCTAACTC	1560	
Db	1501	TAAAGCCTTTGGGACCTCATGGATTA	CTTTCCAAATCTGTCCAACTCAATGGTCTAACTC	1560	
Qy	1561	TAAAGATGGTGGATGATCAAA	CCTTTGATGGAAACCTCTCGGCCAGGAA	1620	
Db	1561	TAAAGATGGTGGATGATCAAA	CCTTTGATGGAAACCTCTCGGCCAGGAA	1620	
Qy	1621	GTTTACCTGGGCTGCCAGCTTCTCATATAGTTTTTTT	TGTGATAAGAAATGECAAAGTTG	1680	
Db	1621	GTTTACCTGGGCTGCCAGCTTCTCATATAGTTTTTTT	TGTGATAAGAAATGECAAAGTTG	1680	
Qy	1681	CTGCTTGCATCTGAAAAATAAAATATATCTAGT	CTCTGCACACTG	1721	-

Db	1681	CTGCTTGCACTCGAATAAATAATACATAGTCCTGCACACTG	1721
RESULT 4			
AAZ33290			
ID	AAZ33290	standard; cDNA; 1721 BP.	
XX	AAZ33290;		
XX			
DT	21-FEB-2000	(first entry)	
XX			
DE	Human heparanase nucleotide sequence.		
XX			
KW	Human; heparanase; hpa; diagnosis; therapy; tumour; cyto		
KW	antidiabetic; immunomodulatory; anti-inflammatory; neph		
KW	metastasis; adenocarcinoma; squamous cell carcinoma; tel		
KW	mesothelioma; melanoma; lymphoma; leukemia; cancer; sep		
KW	inflammation; haemorrhagic nephritis; nephrotic syndrom		
KW	autoimmune disease; anticancer; kidney disease; ds		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	63..1694	
FT		/*tag= a	
FT		/product= "heparanase"	
XX	WO957153-A1.		
XX			
PD	11-NOV-1999.		
XX			
PF	29-APR-1999;	98WO-US009255.	
XX			
PR	01-MAY-1998;	98US-00071739.	
XX			
PA	(INST-) INSIGHT STRATEGY & MARKETING LTD.		
PA	(HADA-) HADASIT MEDICAL RES SERVICES & DEV.		
PA	(PRIE/) FRIEDMAN M M.		
XX			
PI	Pecker I, Vlodaveky I, Friedman Y, Perets T;		
XX			
WP	WI; 2000-052944/04.		
DR	P-PSDB; AAY52990.		
XX			
PT	Heparanase-specific molecular probes useful for diagnos		
PT	e.g. of tumors, and for targeted drug delivery.		
XX			
PS	Example; Page 82-84; 90pp; English.		
XX			
CC	The present invention describes heparanase-specific mol		
CC	useful for methods of detecting heparanase in situ. The		
CC	heparanase antibodies are used to detect or quantify th		
CC	heparanase, for diagnosis and monitoring of diseases (e		
CC	metastasis), for treatment of heparanase-associated dis		
CC	tumours, (adenocarcinoma, squamous cell carcinoma, ter		
CC	mesothelioma, melanoma, lymphoma or leukemia, a solid c		
CC	metastases) derived from liver, prostate, bladder, brea		
CC	colon, skin, intestine, stomach, uterus and pancreas, k		
CC	diabetes and inflammation, haemorrhagic nephritis, neph		
CC	sepsis and inflammation or autoimmune disease), for tar		
CC	delivery (e.g. of anticancer agents) and as research res		
CC	present sequence encodes human heparanase, which is use		
CC	exemplification of the present invention		
XX			
SQ	Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0		
	Query Match	99.9%;	Score 1719.4; DB 3; Leng
	Best Local Similarity	99.9%;	Pred. No. 0;
	Matches 1720; Conservative	0;	Mismatches 1; Indel
OY	1	CTAGAGCTTTGCACTCGCTGCGCGCAGCTGCGGGGGAGCA	

Db 1 CTAGAGCTTTGCACTCTCGCTGCGCGCAGCTGCGGGGGAGCAGCCAGGTGAGCCCA 60
Qy
Db 61 AGATGCTGCTCGCTCGAAGCTCGCTGCGCGCGCGCTGATCTGCTGCTCGTGGGC 120
Qy
Db 61 AGATGCTGCTCGCTCGAAGCTCGCTGCGCGCGCGCTGATCTGCTGCTCGTGGGC 120
Qy
Db 121 CGCTGGGTCCCTCTCCCTGCGCCCTGCGCCCGACCTGCGCAAGCAGCAGACGTCGTGG 180
Qy
Db 121 CGCTGGGTCCCTCTCCCTGCGCCCTGCGCCCGACCTGCGCAAGCAGCAGACGTCGTGG 180
Qy
Db 181 ACCTGGACTCTTCAACAGAGCGCTGCACTGGTGAGCCCTCGTTCCTGCTGCTCA 240
Qy
Db 181 ACCTGGACTCTTCAACAGAGCGCTGCACTGGTGAGCCCTCGTTCCTGCTGCTCA 240
Qy
Db 241 CCATGTGAGCCAACTGGCCAGCAGCCGCGGTTCCTCATCTCTCGGTTCCTCAAGC 300
Qy
Db 241 CCATGTGAGCCAACTGGCCAGCAGCCGCGGTTCCTCATCTCTCGGTTCCTCAAGC 300
Qy
Db 301 TTCTGTACTTGGCCAGAGGCTTGTCTCTGCTGGTACCTGAGGTTTGGTGCCACCAAGACAG 360
Qy
Db 301 TTCTGTACTTGGCCAGAGGCTTGTCTCTGCTGGTACCTGAGGTTTGGTGCCACCAAGACAG 360
Qy
Db 361 ACTTCTTAATTTTCGATCCCAAGAGGAATCAACCTTTGGAAGAGAACTTACTGGCAAT 420
Qy
Db 361 ACTTCTTAATTTTCGATCCCAAGAGGAATCAACCTTTGGAAGAGAACTTACTGGCAAT 420
Qy
Db 421 CTCAGTCAACAGGATATTTGCAATATGCAATATGCAATCCATCTCTGATGTGGAGAGAGT 480
Qy
Db 421 CTCAGTCAACAGGATATTTGCAATATGCAATATGCAATCCATCTCTGATGTGGAGAGAGT 480
Qy
Db 481 TACGGTTGGAATGGCCCTACAGAGCAATTTGCTACTCCGAGAACACTTACAGAAAAAGT 540
Qy
Db 481 TACGGTTGGAATGGCCCTACAGAGCAATTTGCTACTCCGAGAACACTTACAGAAAAAGT 540
Qy
Db 541 TCAAGAACAGCACTTACTCAAGAGCTCTGATAGTGTCTATACACTTTTGCAAACTGCT 600
Qy
Db 541 TCAAGAACAGCACTTACTCAAGAGCTCTGATAGTGTCTATACACTTTTGCAAACTGCT 600
Qy
Db 601 CAGACTGGACTTGTCTTGGCCCTAAATGGTATTAAAGAACAGCAGATTGCGAGTGA 660
Qy
Db 601 CAGACTGGACTTGTCTTGGCCCTAAATGGTATTAAAGAACAGCAGATTGCGAGTGA 660
Qy
Db 661 ACAGTTCTAATGCTCAGTTGCTCTGGACTACTGCTCTTCCAAGGGGTATAACATTTCTT 720
Qy
Db 661 ACAGTTCTAATGCTCAGTTGCTCTGGACTACTGCTCTTCCAAGGGGTATAACATTTCTT 720
Qy
Db 721 GGGAACTAGGCAATGAACCTAACAGTTTCTTAAAGAGGCTGATATTTTCATCAATGGGT 780
Qy
Db 721 GGGAACTAGGCAATGAACCTAACAGTTTCTTAAAGAGGCTGATATTTTCATCAATGGGT 780
Qy
Db 781 CGCAGTTAGGAGAGATTTTATTCAATTGCAATAAATCTTAAGAAAGTCCACCTTCAAAA 840
Qy
Db 781 CGCAGTTAGGAGAGATTTTATTCAATTGCAATAAATCTTAAAGAAAGTCCACCTTCAAAA 840
Qy
Db 841 ATGCAAACTCTATGGTCTGATGTTGCTGAGCTCGAAGAAAGACGCTGAAGATGCTGA 900
Qy
Db 841 ATGCAAACTCTATGGTCTGATGTTGCTGAGCTCGAAGAAAGACGCTGAAGATGCTGA 900
Qy
Db 901 AGAGCTTCTGAAGCTGGTGAGAGAGTGAATTGATTACAGTTACATGGCATCACTACTATT 960
Qy
Db 901 AGAGCTTCTGAAGCTGGTGAGAGAGTGAATTGATTACAGTTACATGGCATCACTACTATT 960
Qy
Db 961 TGAATGGAAGCATGCTACAGAGGAAGATTTTCTAAACCTTGATGATTGACATTTTTTA 1020
Qy
Db 961 TGAATGGAAGCATGCTACAGAGGAAGATTTTCTAAACCTTGATGATTGACATTTTTTA 1020
Qy
Db 1021 TTTCACTCTGCAAAAGTTTTTCCAGGTGGTTGAGAGCAGCAGCTGGCAAGAGGTCT 1080
Qy
Db 1021 TTTCACTCTGCAAAAGTTTTTCCAGGTGGTTGAGAGCAGCAGCTGGCAAGAGGTCT 1080
Qy
Db 1081 GGTAGGAGAAACAGCTCTGCATATGAGCGGAGCGCCCTTGTATCCGACACCTTTG 1140
Qy
Db 1081 GGTAGGAGAAACAGCTCTGCATATGAGCGGAGCGCCCTTGTATCCGACACCTTTG 1140

Qy 1141 CAGCTGGCTTTATGTGGCTGGATAAAATTTGGCCCTGTGAGCCCGGAATGGGAATAGAAAGTGG 1200
Db
Qy 1141 CAGCTGGCTTTATGTGGCTGGATAAAATTTGGCCCTGTGAGCCCGGAATGGGAATAGAAAGTGG 1200
Db
Qy 1201 TGATAGGCAAGTATTCTTTTGGAGCAGGAAACTACCATTTAGTGGATGAAACTTTCGATC 1260
Db
Qy 1261 CTTTACCTGATTATTGGCTATCTCTTCTGTTCAAGAAATTTGGTGGGACCAAGGTGTAA 1320
Db
Qy 1261 CTTTACCTGATTATTGGCTATCTCTTCTGTTCAAGAAATTTGGTGGGACCAAGGTGTAA 1320
Db
Qy 1321 TGCACAGCGTGCAGAGTTCAAAGAGAGGAGCTTCGAGTATACCTTTCATTTGCACAAACA 1380
Db
Qy 1321 TGCACAGCGTGCAGAGTTCAAAGAGAGGAGCTTCGAGTATACCTTTCATTTGCACAAACA 1380
Qy 1381 CTGACAAATCCAAGGTATAAAGAGAGGAGATTAACTCTGTATGCCATAAACTCCATAACG 1440
Db
Qy 1381 CTGACAAATCCAAGGTATAAAGAGAGGAGATTAACTCTGTATGCCATAAACTCCATAACG 1440
Qy 1441 TCACCAAGTACTTTCGCGTTACCTTATCTCTTTCCTAACAGCAAGTGGATAAATACCTTC 1500
Db
Qy 1441 TCACCAAGTACTTTCGCGTTACCTTATCTCTTTCCTAACAGCAAGTGGATAAATACCTTC 1500
Qy 1501 TAAGACCTTTGGACCTCATGGATTACTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560
Db
Qy 1501 TAAGACCTTTGGACCTCATGGATTACTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560
Qy 1561 TAAAGATGGTGGATGATCAAACTTCCACCTTTTAAATGGAAAACTCTCCGGCCAGGAA 1620
Db
Qy 1561 TAAAGATGGTGGATGATCAAACTTCCACCTTTTAAATGGAAAACTCTCCGGCCAGGAA 1620
Qy 1621 GTTCACTGGGCTTCCAGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680
Db
Qy 1621 GTTCACTGGGCTTCCAGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680
Qy 1681 CTGCTTGCATCTGAAATAAAATATATCTAGTCTGCACACTG 1721
Db
Qy 1681 CTGCTTGCATCTGAAATAAAATATATCTAGTCTGCACACTG 1721

RESULT 5
AAA91112
ID AAA91112 standard; DNA; 1721 BP.
XX
XX AAA91112;
XX
XX 20-APR-2001 (first entry)
XX
XX Human heparanase, coding sequence fragment isolated from EST clone.
XX
XX Heparanase; hnhp1; wound healing; angiogenesis; restenosis; Scrape;
XX KW atherosclerosis; inflammation; pulmonary disease; Alzheimer's disease;
XX KW neurodegenerative disease; Creutzfeldt-Jakob disease; viral infection;
XX KW gene therapy; mouse; expressed sequence tag; ds.
OS Homo sapiens.
FN WO200100643-A2.
PN
PD 04-JAN-2001.
XX
XX 19-JUN-2000; 2000WO-IL000358.
XX
XX 25-JUN-1999; 99US-0140801P.
XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX Pecker I, Michal I, Itzhaki H;
XX WPI; 2001-137930/14.
XX

PT New polynucleotides and polypeptides that are distantly homologous to
PT heparanase, useful in wound healing, as well as in gene therapy protocols
XX for angiogenesis, restenosis, atherosclerosis, or inflammation.
PS
XX Example 1; Page 67; 67pp; English.

CC This sequence represents a human heparanase coding sequence clone,
CC isolated from an EST clone. The invention relates to heparanase DNA and
CC protein sequences. The heparanase DNA and protein sequences are useful in
CC wound healing, angiogenesis, restenosis, atherosclerosis, inflammation,
CC pulmonary diseases, neurodegenerative diseases (such as Sclerose,
CC Alzheimer's disease, and Creutzfeldt-Jakob disease) or viral infections.
CC The heparanase coding sequence is particularly useful in gene therapy
XX
SQ Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match 99.98; Score 1719.4; DB 4; Length.1721;
Best Local Similarity 99.98; Pred. No. 0;
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CTAGAGCTTTTCGACTCTCCGCTGCGCGCAGCTGGCGGGGGAGCAGCCAGGTGAGCCCA 60
Db 1 CTAGAGCTTTTCGACTCTCCGCTGCGCGCAGCTGGCGGGGGAGCAGCCAGGTGAGCCCA 60
Qy 61 AGATGCTGCTGCGCTGGAAGCTGCGCTGCGCGCGCGCTGATGCTGCTGCTGCGGC 120
Db 61 AGATGCTGCTGCGCTGGAAGCTGCGCTGCGCGCGCGCTGATGCTGCTGCTGCGGC 120
Qy 121 CGCTGGGTCCTCTCCCTCCGCTGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCG 180
Db 121 CGCTGGGTCCTCTCCCTCCGCTGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCG 180
Qy 181 ACCTGGAGCTTTTCCACCGAGAGCGCTGCACTGCTGAGCGCCCTCGTTCCTGCTGCTCA 240
Db 181 ACCTGGAGCTTTTCCACCGAGAGCGCTGCACTGCTGAGCGCCCTCGTTCCTGCTGCTCA 240
Qy 241 CCATTGAGCGCACTGCGCGCAGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 241 CCATTGAGCGCACTGCGCGCAGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Qy 301 TTGCTACCTTGGCCAGAGGCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 301 TTGCTACCTTGGCCAGAGGCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Qy 361 ACTTCTCTAAATTTTCGATCCCAAGAGGAATCAACTTTTGAAGAGAGAGTACTTGGCAAT 420
Db 361 ACTTCTCTAAATTTTCGATCCCAAGAGGAATCAACTTTTGAAGAGAGAGTACTTGGCAAT 420
Qy 421 CTCAAGTCAACAGGATATTTGCAATATGATCCATCCCTCTCTGATGCTGAGAGAGT 480
Db 421 CTCAAGTCAACAGGATATTTGCAATATGATCCATCCCTCTCTGATGCTGAGAGAGT 480
Qy 481 TAGGTTGGATGCGCTTACAGAGCAATTTGCTTCTCCGAGACACTACAGAGAGT 540
Db 481 TAGGTTGGATGCGCTTACAGAGCAATTTGCTTCTCCGAGACACTACAGAGAGT 540
Qy 541 TCAAGAACAGCAGCTTCTCAAGAGCTCTGTAGATGCTATACACTTTTTCGCAACTGCT 600
Db 541 TCAAGAACAGCAGCTTCTCAAGAGCTCTGTAGATGCTATACACTTTTTCGCAACTGCT 600
Qy 601 CAGGACTGGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 601 CAGGACTGGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Qy 661 ACAGTTCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 661 ACAGTTCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Qy 721 GGGAACTAGGCAATGAACCTTCTTGAAGAGGCTGATATTTTTCATCAATGGGT 780
Db 721 GGGAACTAGGCAATGAACCTTCTTGAAGAGGCTGATATTTTTCATCAATGGGT 780
Qy 781 CGCAGTTAGGAGAGATTTTATTCATTTGCAATAAATCTTCTAAGAAAGTCCACCTTCAAAA 840

RESULT 6

ADG88801

ID ADG88801 standard; cDNA; 1721 BP.

XX

ADG88801;

XX

DT 11-MAR-2004 (first entry)

XX

DE Human hpa cDNA.

Db 781 CGCAGTTAGGAGAGATTTATTTCAATTCATAACTTCTAAGAAAGTCCACCTTCAAAA 840
Qy 841 ATCAAAATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 841 ATCAAAATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Qy 901 AGAGCTTCTGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 AGAGCTTCTGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Qy 961 TGAATGAGCGGACTGCTACCGAGAGATTTTCTAAACCTGATGATTTGGACATTTTAA 1020
Db 961 TGAATGAGCGGACTGCTACCGAGAGATTTTCTAAACCTGATGATTTGGACATTTTAA 1020
Qy 1021 TTTTCATCTGTCAAAAGATTTTCCAGTGGTTCAGAGCAGCAGCCCTGGCAAGAGTCT 1080
Db 1021 TTTTCATCTGTCAAAAGATTTTCCAGTGGTTCAGAGCAGCAGCCCTGGCAAGAGTCT 1080
Qy 1081 GGTAGGAGAAAACAAGCTCTGCAATATGGAGCGGAGCGCTTGTCTATCCGACACCTTTG 1140
Db 1081 GGTAGGAGAAAACAAGCTCTGCAATATGGAGCGGAGCGCTTGTCTATCCGACACCTTTG 1140
Qy 1141 CAGCTGGCTTATGCTGGCTGGATAAATTTGGGCTGTGAGCGCGAGCGCTTGTCTATCCGACACCTTTG 1200
Db 1141 CAGCTGGCTTATGCTGGCTGGATAAATTTGGGCTGTGAGCGCGAGCGCTTGTCTATCCGACACCTTTG 1200
Qy 1201 TGAATGAGCGGAGATTTCTTTTGGAGCAGGAAATACCATTTAGTGGATGAAATCTTCGATC 1260
Db 1201 TGAATGAGCGGAGATTTCTTTTGGAGCAGGAAATACCATTTAGTGGATGAAATCTTCGATC 1260
Qy 1261 CTTTACCTGATTTAGCTGCTATCTCTTCTGTTCAAGAAAATTTGGTGGGACCAAGGTGTAA 1320
Db 1261 CTTTACCTGATTTAGCTGCTATCTCTTCTGTTCAAGAAAATTTGGTGGGACCAAGGTGTAA 1320
Qy 1321 TGGCAGCTGTCAGGTTTCAAGAGAGAGGAGCTTCGAGTATACCTTCATTCGACAAACA 1380
Db 1321 TGGCAGCTGTCAGGTTTCAAGAGAGAGGAGCTTCGAGTATACCTTCATTCGACAAACA 1380
Qy 1381 CTGCAATCAAGGTATTAAGAGAGAGATTTAACTCTGATGCTAATAAACCCTCCATAACG 1440
Db 1381 CTGCAATCAAGGTATTAAGAGAGAGATTTAACTCTGATGCTAATAAACCCTCCATAACG 1440
Qy 1441 TCACCAAGTACTTTGCGGTTACCCCTATCCCTTTTCTAACAGCAAGTGGATTAACCTTC 1500
Db 1441 TCACCAAGTACTTTGCGGTTACCCCTATCCCTTTTCTAACAGCAAGTGGATTAACCTTC 1500
Qy 1501 TAAGACCTTTGGACCTGATGATTTCTGCAATCTGCTCAACTGCTCAATGGTCTAACTC 1560
Db 1501 TAAGACCTTTGGACCTGATGATTTCTGCAATCTGCTCAACTGCTCAATGGTCTAACTC 1560
Qy 1561 TAAAGATGTTGGATGATCAAACTTCCACCTTTAATGGAATAAACCCTCCGCGCCAGGAA 1620
Db 1561 TAAAGATGTTGGATGATCAAACTTCCACCTTTAATGGAATAAACCCTCCGCGCCAGGAA 1620
Qy 1621 GTTCACTGGGCTTGGCAGCTTTCTCATATAGTTTTTTTGTGTAAGAAATGCCAAAGTTG 1680
Db 1621 GTTCACTGGGCTTGGCAGCTTTCTCATATAGTTTTTTTGTGTAAGAAATGCCAAAGTTG 1680
Qy 1681 CTGCTTGCATCTGAAATAAATAATATAGTCTGCTGACACTG 1721
Db 1681 CTGCTTGCATCTGAAATAAATAATATAGTCTGCTGACACTG 1721

RESULT 6

ADG88801

ID ADG88801 standard; cDNA; 1721 BP.

XX

ADG88801;

XX

DT 11-MAR-2004 (first entry)

XX

DE Human hpa cDNA.

XX Wound healing; heparanase; ulcer; burn; laceration; surgical incision;
KW necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy;
KW gene; ss.
XX
XX Homo sapiens.
XX OS
XX Location/Qualifiers
FH 63. .1694
FT /*tag= a
FT /product= "Human hpa protein"
XX
XX US2003161823-A1.
XX
XX 28-AUG-2003.
XX
XX 14-JAN-2003; 2003US-00341592.
XX
XX 31-AUG-1998; 98WO-US017954.
XX 01-MAR-1999; 99US-00258892.
XX 06-FEB-2001; 2001US-00776874.
XX 05-SEP-2001; 2001US-IL000830.
XX 19-NOV-2001; 2001US-00988113.
XX
XX (ILAN/) ILAN N.
XX (VLOD/) VLODAVSKY I.
XX (YACO/) YACOBY-ZEEVI O.
XX (PECK/) PECKER I.
XX (FEIN/) FEINSTEIN E.
XX
XX Ilan N, Vlodavsky I, Yacoby-Zeevi O, Pecker I, Feinstein E;
XX
XX WPI; 2003-897910/82.
XX P-PSDB; ADG88800.
XX
XX Composition for treating a wound comprising recombinant heparanase is
XX useful to induce or accelerate wound healing and induce or accelerate
XX angiogenesis.
XX
XX Example 1; SEQ ID NO 11; 143pp; English.
XX
XX The present invention relates to methods and compositions for inducing
XX and/or accelerating wound healing via the catalytic activity of
XX heparanase. The invention is used to induce or accelerate a healing
XX process, particularly of an ulcer, burn, laceration, surgical incision,
XX necrosis, pressure wound, diabetic ulcer and to induce or accelerate
XX angiogenesis. The present sequence is human hpa cDNA.
XX
XX Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;
XX
XX Query Match 99.9%; Score 1719.4; DB 10; Length 1721;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 CTAGAGCTTTTCGACTCTCCGCTGCGCGGAGCTGGCGGGGAGCAGCCAGTGGAGCCCA 60
XX
XX 1 CTAGAGCTTTTCGACTCTCCGCTGCGCGGAGCTGGCGGGGAGCAGCCAGTGGAGCCCA 60
XX
XX 61 AGATGCTGCTGCTCGAAGCTGCGCTGCGCGCGCGCGCTGATGCTGCTCTGGGGC 120
XX
XX 61 AGATGCTGCTGCTCGAAGCTGCGCTGCGCGCGCGCGCTGATGCTGCTCTGGGGC 120
XX
XX 121 CGCTGGGTCCCTCTCCGCTGGCGCGCTGCGCGCGCGCGCTGATGCTGCTGCTGG 180
XX
XX 121 CGCTGGGTCCCTCTCCGCTGGCGCGCTGCGCGCGCGCGCTGATGCTGCTGCTGG 180
XX
XX 181 ACCTGGGACTTCTTCCAGCAGGAGCGCTGCAACCTGGTGAGCCCTCGTCTGTCGCTCA 240
XX
XX 181 ACCTGGGACTTCTTCCAGCAGGAGCGCTGCAACCTGGTGAGCCCTCGTCTGTCGCTCA 240
XX
XX 241 CCATTGACGCCAAGCTGGCCACGAGCGCGGGTTCCTCATCTCTGGGGTTCCTCAAGC 300
XX
XX 241 CCAFTGACGCCAAGCTGGCCACGAGCGCGGGTTCCTCATCTCTGGGGTTCCTCAAGC 300
XX

Qy 301 TTCTGTACCTTTGGCCAGAGGCTTGTCTCTCTGCTACCTGAGGTTTGGTGGCCACCAAGACAG 360
Db 301 TTCTGTACCTTTGGCCAGAGGCTTGTCTCTCTGCTACCTGAGGTTTGGTGGCCACCAAGACAG 360
Qy 361 ACTTCTTAATTTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGAAAGTTTACTTGGCAAT 420
Db 361 ACTTCTTAATTTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGAAAGTTTACTTGGCAAT 420
Qy 421 CTCAAGTCAACCCAGGATATTTTGCAAAATATGGATCCATCCCTCTCTGATGTGGAGGAGAGT 480
Db 421 CTCAAGTCAACCCAGGATATTTTGCAAAATATGGATCCATCCCTCTCTGATGTGGAGGAGAGT 480
Qy 481 TACGGTTTGGAAATGGCCCTACACAGAGCAATTTGCTACTCCGAGACACATACCAGAAAAGT 540
Db 481 TACGGTTTGGAAATGGCCCTACACAGAGCAATTTGCTACTCCGAGACACATACCAGAAAAGT 540
Qy 541 TCAAGAACACGACCTACTCTCAAGAAAGCTCTGTAGATGTCTATACACTTTTTCGAAACTGCT 600
Db 541 TCAAGAACACGACCTACTCTCAAGAAAGCTCTGTAGATGTCTATACACTTTTTCGAAACTGCT 600
Qy 601 CAGGACTGGACTTGTATCTTTTGGGCTAAATGGCTTATTAAGAACAGCAGATTTTGCAGTGGGA 660
Db 601 CAGGACTGGACTTGTATCTTTTGGGCTAAATGGCTTATTAAGAACAGCAGATTTTGCAGTGGGA 660
Qy 661 ACAGTTCTAATGTCTCAGTTGCTCTCTGACTACTGCTCTTCCAGGGGTATTAACATTTCTT 720
Db 661 ACAGTTCTAATGTCTCAGTTGCTCTCTGACTACTGCTCTTCCAGGGGTATTAACATTTCTT 720
Qy 721 GGGAACTAGGCAATGAACCTAAACAGTTTCTTAAAGAGGCTGATATTTTTCATCAATGGGT 780
Db 721 GGGAACTAGGCAATGAACCTAAACAGTTTCTTAAAGAGGCTGATATTTTTCATCAATGGGT 780
Qy 781 CGCAGTTAGGAGAAAGATTTTATTCATTTGTCATAACTTCTTAAGAAAGTCCACCTTCAAAA 840
Db 781 CGCAGTTAGGAGAAAGATTTATTTCAATTTGTCATAAATCTTCTAAGAAAGTCCACCTTCAAAA 840
Qy 841 ATGCAAAACTCTATGCTCTGATGTTGGTTCAGCTCGAAGAAAGACGGCTGAAGTCTGA 900
Db 841 ATGCAAAACTCTATGCTCTGATGTTGGTTCAGCTCGAAGAAAGACGGCTGAAGTCTGA 900
Qy 901 AGAGCTTCTTGAAGGCTGGTGGAGAGTGTGATTCAGTTTACATGAGCATCAGTACTATT 960
Db 901 AGAGCTTCTTGAAGGCTGGTGGAGAGTGTGATTCAGTTTACATGAGCATCAGTACTATT 960
Qy 961 TGAATGGACGGACTGCTTACAGGGAAGATTTCTAAACCTCTGATGTATGGACATTTTAA 1020
Db 961 TGAATGGACGGACTGCTTACAGGGAAGATTTCTAAACCTCTGATGTATGGACATTTTAA 1020
Qy 1021 TTTTCATCTGTGCAAAAAGTTTTCAGGTGGTTGAGAGCACCGGCTGGCAAGAGGCTCT 1080
Db 1021 TTTTCATCTGTGCAAAAAGTTTTCAGGTGGTTGAGAGCACCGGCTGGCAAGAGGCTCT 1080
Qy 1081 GGTTAGGAGAAAACAAGCTCTGTCATATGAGGCGGAGCGCCCTTGTATCCGACACCTTTG 1140
Db 1081 GGTTAGGAGAAAACAAGCTCTGTCATATGAGGCGGAGCGCCCTTGTATCCGACACCTTTG 1140
Qy 1141 CAGTGGCTTTTATGTGGCTGGATAAATTTGGGCTGTGAGCCCGAATAGGAAGTGG 1200
Db 1141 CAGTGGCTTTTATGTGGCTGGATAAATTTGGGCTGTGAGCCCGAATAGGAAGTGG 1200
Qy 1201 TGATGAGGCAAGTATTTCTTTGGAGCAGGAACCTACCAATTTAGTGGATGAAAACCTTCGATC 1260
Db 1201 TGATGAGGCAAGTATTTCTTTGGAGCAGGAACCTACCAATTTAGTGGATGAAAACCTTCGATC 1260
Qy 1261 CTTTACCTGATTTATGGCTATCTTCTGTTCAGAAATTTGGTGGGCAACAAGGTGTAA 1320
Db 1261 CTTTACCTGATTTATGGCTATCTTCTGTTCAGAAATTTGGTGGGCAACAAGGTGTAA 1320
Qy 1321 TGGCAAGCGTGCAGGTTTCAAGAGAGGAAGTTCGAGTATACCTTTCATTTGCAAAAACA 1380
Db 1321 TGGCAAGCGTGCAGGTTTCAAGAGAGGAAGTTCGAGTATACCTTTCATTTGCAAAAACA 1380

Qy 1381 CTGACAAATCCAAAGTATAAAGAGGAGATTAACTCTGTATGCGCATAAACCTCCATAACG 1440
Db 1381 CTGACAAATCCAAAGTATAAAGAGGAGATTAACTCTGTATGCGCATAAACCTCCATAACG 1440
Qy 1441 TCACCAAGTACTGGCGGTACCCCTATCTTTTCTACCAAGCAAGTGGATATACCTTC 1500
Db 1441 TCACCAAGTACTGGCGGTACCCCTATCTTTTCTACCAAGCAAGTGGATATACCTTC 1500
Qy 1501 TAAGACCTTTGGGACCTCATGGATTACTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560
Db 1501 TAAGACCTTTGGGACCTCATGGATTACTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560
Qy 1561 TAAAGATGGTGGATGATCAAAACCTTGGACCTTTAATGGAAAAACCTCTCGGCCAGGAA 1620
Db 1561 TAAAGATGGTGGATGATCAAAACCTTGGACCTTTAATGGAAAAACCTCTCGGCCAGGAA 1620
Qy 1621 GTTCACATGGGCTTCCAGCTTTCTCATATAGTTTTTTTGTATGAAGAAATGCCAAAGTTG 1680
Db 1621 GTTCACATGGGCTTCCAGCTTTCTCATATAGTTTTTTTGTATGAAGAAATGCCAAAGTTG 1680
Qy 1681 CTGCTTGCATCGAAAAATAAATATACTAGTCTCGACACTG 1721
Db 1681 CTGCTTGCATCGAAAAATAAATATACTAGTCTCGACACTG 1721
RESULT 7
ADG88799
ID ADG88799 standard; cDNA; 1721 BP.
XX
AC ADG88799;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human hpa cDNA.
XX
KW Wound healing; heparanase; ulcer; burn; laceration; surgical incision;
KW necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy;
KW gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 63..1694
FT FT /*tag= a
FT FT /product= "Human hpa protein"
XX
PN US2003161823-A1.
XX
PD 28-AUG-2003.
XX
PF 14-JAN-2003; 2003US-00341582.
XX
PR 31-AUG-1998; 98WO-US017954.
PR 01-MAR-1999; 99US-00258892.
PR 06-FEB-2001; 2001US-00776874.
PR 05-SEP-2001; 2001WO-IL000830.
PR 19-NOV-2001; 2001US-00988113.
XX
PA (ILAN/) ILAN N.
PA (VLOD/) VLODAVSKY I.
PA (YACO/) YACOBY-ZEEVI O.
PA (PECK/) PECKER I.
PA (FEIN/) FEINSTEIN E.
XX
FI Ilan N, Vlodavsky I, Yacoby-Zeevi O, Pecker I, Feinstein E;
XX
DR WPI; 2003-897910/82.
DR P-PSDB; ADG88800.
XX
XX Composition for treating a wound comprising recombinant heparanase is
XX useful to induce or accelerate wound healing and induce or accelerate
XX angiogenesis.

PS Claim 4; SEQ ID NO 9; 143pp; English.
XX
CC The present invention relates to methods and compositions for inducing
CC and/or accelerating wound healing via the catalytic activity of
CC heparanase. The invention is used to induce or accelerate a healing
CC process, particularly of an ulcer, burn, laceration, surgical incision,
CC necrosis, pressure wound, diabetic ulcer and to induce or accelerate
CC angiogenesis. The present sequence is human hpa cDNA.
XX
SQ Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;
Query Match 99.9%; Score 1719.4; DB 10; Length 1721;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CTAGAGCTTTCGACTCTCGCGGAGAGCTGGCGGGGAGAGCAGCAGGTGAGGCCA 60
Db 1 CTAGAGCTTTCGACTCTCGCGGAGAGCTGGCGGGGAGAGCAGCAGGTGAGGCCA 60
Qy 61 AGATGCTGTGCGCTCGAAGCCTGCGCTGCCCGCGCTGATGCTGCTCTCTGGGC 120
Db 61 AGATGCTGTGCGCTCGAAGCCTGCGCTGCCCGCGCTGATGCTGCTCTCTGGGC 120
Qy 121 CGCTGGGTCCCTCTCCCTGGCGCCCTGCCCGAGCTTGGCAAGCAGCAGGTGCTG 180
Db 121 CGCTGGGTCCCTCTCCCTGGCGCCCTGCCCGAGCTTGGCAAGCAGCAGGTGCTG 180
Qy 181 ACCTGGACTTCTTCCACCGAGGCGCTGCGACCTGTGGAGCCCTCTGCTCTCGTCA 240
Db 181 ACCTGGACTTCTTCCACCGAGGCGCTGCGACCTGTGGAGCCCTCTGCTCTCGTCA 240
Qy 241 CCATTGACGCCAACCTGGGCCACCGCGGTTCTCTCATCTCTGGGTTCTCCAAAGC 300
Db 241 CCATTGACGCCAACCTGGGCCACCGCGGTTCTCTCATCTCTGGGTTCTCCAAAGC 300
Qy 301 TTGCTACCTTGGCCAGAGGCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 301 TTGCTACCTTGGCCAGAGGCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Qy 361 ACTTCTTAATTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGAGTTACTGGCAAT 420
Db 361 ACTTCTTAATTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGAGTTACTGGCAAT 420
Qy 421 CTCAGTCAACAGGATATTTGCAATATGATCCATCCCTCTCTGATGTGGAGAGAGT 480
Db 421 CTCAGTCAACAGGATATTTGCAATATGATCCATCCCTCTCTGATGTGGAGAGAGT 480
Qy 481 TAGCGTTGGAATGGCCCTTACAGAGCAATTTGCTACTCCGAGAACACTACAGAAAAAGT 540
Db 481 TAGCGTTGGAATGGCCCTTACAGAGCAATTTGCTACTCCGAGAACACTACAGAAAAAGT 540
Qy 541 TCAAGAACAGCACCTACTCTCAAGAGGCTCTGTAGATGTGTATACATTTTGCACAACTGCT 600
Db 541 TCAAGAACAGCACCTACTCTCAAGAGGCTCTGTAGATGTGTATACATTTTGCACAACTGCT 600
Qy 601 CAGGACTGGACTTGTATCTTTGGCTAAATGCGTTATTAAGAACAGCAGATTTGCAAGTGA 660
Db 601 CAGGACTGGACTTGTATCTTTGGCTAAATGCGTTATTAAGAACAGCAGATTTGCAAGTGA 660
Qy 661 ACAGTCTTAATGTCTCAGTTGCTCTCGGACTACTGCTCTTCCAAAGGGGTATAACATTTCTT 720
Db 661 ACAGTCTTAATGTCTCAGTTGCTCTCGGACTACTGCTCTTCCAAAGGGGTATAACATTTCTT 720
Qy 721 GGAACCTAGGCAATGAACCTTAACAGTTTCTTAAAGAGGCTGATATTTTCAATCAATGGGT 780
Db 721 GGAACCTAGGCAATGAACCTTAACAGTTTCTTAAAGAGGCTGATATTTTCAATCAATGGGT 780
Qy 781 CGCAGTTAGGAGAGATTTTATTAATGATATAAATTTCTAAGAAAGTCCACCTTCAAAA 840
Db 781 CGCAGTTAGGAGAGATTTTATTAATGATATAAATTTCTAAGAAAGTCCACCTTCAAAA 840
Qy 841 ATCCAAACTCTATGCTGCTGATGTTGGTCCAGCTCGAAGAAAGACGGCTAAGATGCTGA 900
Db 841 ATCCAAACTCTATGCTGCTGATGTTGGTCCAGCTCGAAGAAAGACGGCTAAGATGCTGA 900

Db 841 ATGCAAACTCTATGTCCTGATGTTGGTCAGCCCTCGAAGAAAGACGGCTAAGATGCTGA 900
Qy 901 AGAGCTTCCTGAGCGTGGTGGAGAGTGATTGATTACAGTTACATGCGATCAGTACTATT 960
Db 901 AGAGCTTCCTGAGCGTGGTGGAGAGTGATTGATTACAGTTACATGCGATCAGTACTATT 960
Qy 961 TGAATGGACGAGCTGCTACCAAGGGAAGATTCTTAAACCCCTGATGTTATGGACATTTTTTA 1020
Db 961 TGAATGGACGAGCTGCTACCAAGGGAAGATTCTTAAACCCCTGATGTTATGGACATTTTTTA 1020
Qy 1021 TTTCAATCTGTGCAAAAAGTTTTTCCAGGTGGTTGAGAGCACCAGCGCTGGCAAGAGTCT 1080
Db 1021 TTTCAATCTGTGCAAAAAGTTTTTCCAGGTGGTTGAGAGCACCAGCGCTGGCAAGAGTCT 1080
Qy 1081 GGTTAGGAGAACAGCTCTGCATATGGAGCGGAGCGCCCTTCTATCCGACACCTTTTG 1140
Db 1081 GGTTAGGAGAACAGCTCTGCATATGGAGCGGAGCGCCCTTCTATCCGACACCTTTTG 1140
Qy 1141 CAGCTGGCTTTATGTGGCTGGATAAATTTGGCCCTGTGAGCCCGAATGGGAATAGAAGTGG 1200
Db 1141 CAGCTGGCTTTATGTGGCTGGATAAATTTGGCCCTGTGAGCCCGAATGGGAATAGAAGTGG 1200
Qy 1201 TGATGAGCAAGTATTCTTTGGAGCAGGAACCTACCAATTTAGTGGATGAAACCTTCGATC 1260
Db 1201 TGATGAGCAAGTATTCTTTGGAGCAGGAACCTACCAATTTAGTGGATGAAACCTTCGATC 1260
Qy 1261 CTTTACCTGATATGCTATCTCTCTGTTCAAGAAATTTGGTGGCACCAAGTGTTAA 1320
Db 1261 CTTTACCTGATATGCTATCTCTCTGTTCAAGAAATTTGGTGGCACCAAGTGTTAA 1320
Qy 1321 TGGCAAGCGTCCAAAGGTTCAAAGAGAAGAGCTTCAGATATACCTTCATTGCAACAACA 1380
Db 1321 TGGCAAGCGTCCAAAGGTTCAAAGAGAAGAGCTTCAGATATACCTTCATTGCAACAACA 1380
Qy 1381 CTGCAATCCAAAGGTATAAAGAGGAGATTTAACTCTGTATGCCATAAACCTCCATAAG 1440
Db 1381 CTGCAATCCAAAGGTATAAAGAGGAGATTTAACTCTGTATGCCATAAACCTCCATAAG 1440
Qy 1441 TCACCAAGTACTTGGGTTACCTTATCCCTTTCTTAACAAGCAAGTGGATAAATACCTTC 1500
Db 1441 TCACCAAGTACTTGGGTTACCTTATCCCTTTCTTAACAAGCAAGTGGATAAATACCTTC 1500
Qy 1501 TAAGACCTTTGGGACCTCATGGATTACTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560
Db 1501 TAAGACCTTTGGGACCTCATGGATTACTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560
Qy 1561 TAAAGATGGTGGATGATCAAAACCTTGGCACCTTTAATGGAATAAACCTCTCCGGCCAGAA 1620
Db 1561 TAAAGATGGTGGATGATCAAAACCTTGGCACCTTTAATGGAATAAACCTCTCCGGCCAGAA 1620
Qy 1621 GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680
Db 1621 GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680
Qy 1681 CTGCTTGATCTGAAATAAATAATACTAGTCCCTGACACTG 1721
Db 1681 CTGCTTGATCTGAAATAAATAATACTAGTCCCTGACACTG 1721

RESULT 8
ADL16380
ID ADL16380 standard; cDNA; 1721 BP.
XX
AC ADL16380;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heparanase partial cDNA #2.
XX
KW Human; ss; heparanase; gene; heparanase-dependent cancer; cancer;
KW autoimmune reaction; inflammation; chromosome 4.
XX
OS Homo sapiens.

XX US2003236215-A1.
PN 25-DEC-2003.
XX
PF 09-JUN-2003; 2003US-00456573.
XX
XX 31-AUG-1998; 98WO-US017954.
PR 01-MAR-1999; 99US-00258892.
PR 08-NOV-1999; 99US-00435739.
XX
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX
PI Pecker I, Vlodavsky I, Feinstein E;
XX WPI; 2004-070610/07.
DR
XX
PT New antisense oligonucleotide hybridizable with a polynucleotide encoding
PT a polypeptide with heparanase activity, useful for treating diseases such
PT as cancer and autoimmune disorders.
XX
PS Example 1; SEQ ID NO 11; 108pp; English.
XX
CC The invention relates to an antisense oligonucleotide (ASO) comprising a
CC polynucleotide or a polynucleotide analogue of at least 10 bases being
CC hybridisable in vivo, under physiological conditions, with a portion of
CC a polynucleotide strand encoding a polypeptide having heparanase
CC catalytic activity. Also included are a method of in vivo downregulating
CC heparanase activity (comprising administering the ASO in vivo), a method
CC of treating a subject suffering from a pathological condition
CC (characterised by heparanase activity, comprising administering ASO to
CC the subject), a pharmaceutical composition comprising the ASO and a
CC carrier, an antisense nucleic acid construct (comprising a promoter
CC sequence and a polynucleotide sequence directing the synthesis of an
CC antisense RNA sequence of at least 10 bases being hybridisable in vivo,
CC under physiological conditions, with a polynucleotide strand encoding a
CC polypeptide having heparanase catalytic activity), a method of in vivo
CC downregulating heparanase activity (comprising administering in vivo the
CC antisense nucleic acid construct), a pharmaceutical composition
CC comprising the antisense nucleic acid construct and a carrier, and an
CC antisense oligonucleotide comprising a polynucleotide or a polynucleotide
CC analogue of at least 10 bases being hybridisable in vivo, under
CC physiological conditions, with a portion of a polynucleotide strand being
CC characterised by forming at least a portion of an untranslated region
CC (UTR) for a polynucleotide strand encoding a polypeptide having
CC heparanase catalytic activity. The methods and compositions of the
CC present invention are useful for the prevention and/or treatment of
CC diseases or conditions associated with aberrant heparanase activity, such
CC as heparanase-dependent cancer, cancer, autoimmune reaction and
CC inflammation. The gene for human heparanase is located on chromosome 4.
CC The present sequence is a human heparanase cDNA.
XX
SQ Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;
Qy Query Match 99.9%; Score 1719.4; DB 12; Length 1721;
Db Best Local Similarity 99.9%; Pred. No. 0;
Qy Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 CTAGAGCTTTTCGACTCTCCGCTGCGCGGAGCTGGCGGGGAGCAGCCAGGTGAGCCCA 60
Qy 61 AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCGCTGATGCTGCTCTCTCTGGGC 120
Db 61 AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCGCTGATGCTGCTCTCTCTGGGC 120
Qy 121 CGCTGGGTCCCTCTCCCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCG 180
Db 121 CGCTGGGTCCCTCTCTCCCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTG 180
Qy 181 ACCTGGACTTCTTTCACCCAGGAGCGCTGCACCTGGTGAAGCCCTCTCTCTCTCTCTCA 240

Db 181 ACCTGAGACTTCTTCAACCGAGAGCCGCTGCACCTGGTGAGCCCTCCTGTTCTGTCCTGCA 240
Qy 241 CCATTGACGCAACCTGCGCACGACCGCGGTTCTCATCTCCTCGGTTCTCGAAAGC 300
Db 241 CCATTGACGCAACCTGCGCACGACCGCGGTTCTCATCTCCTCGGTTCTCGAAAGC 300
Qy 301 TTCGTACTTGGCCAGAGGCTTGTCTCTCGCTACCTGAGTTTGGTGCGACCAAGACAG 360
Db 301 TTCGTACTTGGCCAGAGGCTTGTCTCTCGCTACCTGAGTTTGGTGCGACCAAGACAG 360
Qy 361 ACTTCTTAATTTTCGATCCCAAGAGGAACTCAACCTTTGAGAGAGTACTTACTGCAAT 420
Db 361 ACTTCTTAATTTTCGATCCCAAGAGGAACTCAACCTTTGAGAGAGTACTTACTGCAAT 420
Qy 421 CTCAAGTCAACAGGATTTTGCAGATATGATCCATCCCTCTCTGATGTGGAGAGAGT 480
Db 421 CTCAAGTCAACAGGATTTTGCAGATATGATCCATCCCTCTCTGATGTGGAGAGAGT 480
Qy 481 TAGCGTTGGAATGCCCCCTACAGAGCAATTTGCTACTCCGAGAACACTA 540
Db 481 TAGCGTTGGAATGCCCCCTACAGAGCAATTTGCTACTCCGAGAACACTA 540
Qy 541 TCAGAACAGCACTACTCAAGAGCTCTGTAGATGCTATACACTTTTGCACACTGCT 600
Db 541 TCAGAACAGCACTACTCAAGAGCTCTGTAGATGCTATACACTTTTGCACACTGCT 600
Qy 601 CAGGACTGGACTTGATCTTTGGCCCTAAATGCGTTATTAAAGAACAGCAGATTTGCGAGTGA 660
Db 601 CAGGACTGGACTTGATCTTTGGCCCTAAATGCGTTATTAAAGAACAGCAGATTTGCGAGTGA 660
Qy 661 ACAGTTCTAATGCTCAGTTGCTCTGCACTACTGCTCTTCCAGGGGTTAACAATTTCTT 720
Db 661 ACAGTTCTAATGCTCAGTTGCTCTGCACTACTGCTCTTCCAGGGGTTAACAATTTCTT 720
Qy 721 GGGAACTAGGCAATGAACCTTAAACAGTTTCCCTTAAGAGGCTGATATTTTATCAATGGGT 780
Db 721 GGGAACTAGGCAATGAACCTTAAACAGTTTCCCTTAAGAGGCTGATATTTTATCAATGGGT 780
Qy 781 CGCAGTTAGGAGAGATTTTATTCAATGTCATTAACCTTCTAAGAAAGCTCCACCTTCAAAA 840
Db 781 CGCAGTTAGGAGAGATTTTATTCAATGTCATTAACCTTCTAAGAAAGCTCCACCTTCAAAA 840
Qy 841 ATGCAAAATCTATGCTGCTGATGTTGGTTCAGCCTCGAAGAAAGACGCGCTAAGATGCTGA 900
Db 841 ATGCAAAATCTATGCTGCTGATGTTGGTTCAGCCTCGAAGAAAGACGCGCTAAGATGCTGA 900
Qy 901 AGAGCTTCTGAAGGCTGGTGGAGAGTGTGATTCAGTTACATGCGATCACTACTATT 960
Db 901 AGAGCTTCTGAAGGCTGGTGGAGAGTGTGATTCAGTTACATGCGATCACTACTATT 960
Qy 961 TGAATGACGAGCTGCTACAGGGGAAGATTTTCTAAACCTGTATGATGACATTTTAA 1020
Db 961 TGAATGACGAGCTGCTACAGGGGAAGATTTTCTAAACCTGTATGATGACATTTTAA 1020
Qy 1021 TTTTCATCTGTGCAAAAAGTTTTCAGGTGTTTGAGAGCACACAGGCTTGGCAAGAGTCT 1080
Db 1021 TTTTCATCTGTGCAAAAAGTTTTCAGGTGTTTGAGAGCACACAGGCTTGGCAAGAGTCT 1080
Qy 1081 GGTAGAGAAACAGCTCTGCATATGAGAGCGGAGCGCTTGTCTATCGACACCTTTG 1140
Db 1081 GGTAGAGAAACAGCTCTGCATATGAGAGCGGAGCGCTTGTCTATCGACACCTTTG 1140
Qy 1141 CAGCTGCTTTATGTGCTGATAAATTTGGGCTGTGCGCCGATGGAATGAGTGG 1200
Db 1141 CAGCTGCTTTATGTGCTGATAAATTTGGGCTGTGCGCCGATGGAATGAGTGG 1200
Qy 1201 TGATGAGCAAGTATTTCTTGGAGCAGGAACTACCATTTAGTGGATGAAAACCTTCGATC 1260
Db 1201 TGATGAGCAAGTATTTCTTGGAGCAGGAACTACCATTTAGTGGATGAAAACCTTCGATC 1260
Qy 1261 CTTTACCTGATTTATGGCTATCTCTTCTGTTCAAGAAATTTGGTGGGACCAAGGTGTAA 1320
Db 1261 CTTTACCTGATTTATGGCTATCTCTTCTGTTCAAGAAATTTGGTGGGACCAAGGTGTAA 1320

Qy 1321 TGGCAAGCGTGCAGGTTTCAAGAGAGGAAGCTTCGAGTATACCTTTCAATTGCACAAAACA 1380
Db 1321 TGGCAAGCGTGCAGGTTTCAAGAGAGGAAGCTTCGAGTATACCTTTCAATTGCACAAAACA 1380
Qy 1381 CTGACAAATCAAGGTATAAAGAGGAGATTTAACTCTGTATGCGATAAACCTCCATAAAG 1440
Db 1381 CTGACAAATCAAGGTATAAAGAGGAGATTTAACTCTGTATGCGATAAACCTCCATAAAG 1440
Qy 1441 TCACCAAGTACTTGGCGTTACCTTATCTTCTAAACAGCAAGTGGATAAATACCTTC 1500
Db 1441 TCACCAAGTACTTGGCGTTACCTTATCTTCTAAACAGCAAGTGGATAAATACCTTC 1500
Qy 1501 TAAGACCTTTGGGACCTCATGGAATTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560
Db 1501 TAAGACCTTTGGGACCTCATGGAATTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560
Qy 1561 TAAAGATGTGGATGATCAAACTTGGCACCTTTTAAATGGAAGAAACCTCTCCGGCCAGGAA 1620
Db 1561 TAAAGATGTGGATGATCAAACTTGGCACCTTTTAAATGGAAGAAACCTCTCCGGCCAGGAA 1620
Qy 1621 GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680
Db 1621 GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680
Qy 1681 CTGCTTGGCATCTGAAATTAATAATATATAGTCTGCTGACACTG 1721
Db 1681 CTGCTTGGCATCTGAAATTAATAATATATAGTCTGCTGACACTG 1721

RESULT 9
ADL16378
ID ADL16378 standard; cDNA; 1721 BP.
XX
AC ADL16378;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heparanase partial cDNA #1.
XX
KW Human; ss; heparanase; gene; heparanase-dependent cancer; cancer;
KW autoimmune reaction; inflammation; chromosome 4.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 3'UTR 1695..1721
FT /*tag= a
FT /note= "Claimed in claim 20"
XX
PN US2003236215-A1.
XX
PD 25-DEC-2003.
XX
PF 09-JUN-2003; 2003US-00456573.
XX
PR 31-AUG-1998; 98WO-US017954.
PR 01-MAR-1999; 99US-00258892.
PR 08-NOV-1999; 99US-00435739.
XX
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX
PI Pecker I, Vlodavsky I, Feinstein E;
XX
DR WPI; 2004-070610/07.
XX
PT New antisense oligonucleotide hybridizable with a polynucleotide encoding
PT a polypeptide with heparanase activity, useful for treating diseases such
PT as cancer and autoimmune disorders.
XX
PS Claim 2; SEQ ID NO 9; 108pp; English.
XX

CC The invention relates to an antisense oligonucleotide (ASO) comprising a
CC polynucleotide or a polynucleotide analogue of at least 10 bases being
CC hybridisable *in vivo*, under physiological conditions, with a portion of
CC a polynucleotide strand encoding a polypeptide having heparanase
CC catalytic activity. Also included are a method of *in vivo* downregulating
CC heparanase activity (comprising administering the ASO *in vivo*), a method
CC of treating a subject suffering from a pathological condition
CC (characterised by heparanase activity, comprising administering ASO to
CC the subject), a pharmaceutical composition comprising the ASO and a
CC carrier, an antisense nucleic acid construct (comprising a promoter
CC sequence and a polynucleotide sequence directing the synthesis of an
CC antisense RNA sequence of at least 10 bases being hybridisable *in vivo*,
CC under physiological conditions, with a polynucleotide strand encoding a
CC polypeptide having heparanase catalytic activity), a method of *in vivo*
CC downregulating heparanase activity (comprising administering *in vivo* the
CC antisense nucleic acid construct), a pharmaceutical composition
CC comprising the antisense nucleic acid construct and a carrier, and an
CC antisense oligonucleotide comprising a polynucleotide or a polynucleotide
CC analogue of at least 10 bases being hybridisable *in vivo*, under
CC physiological conditions, with a portion of a polynucleotide strand being
CC characterised by forming at least a portion of an untranslated region
CC (UTR) for a polynucleotide strand encoding a polypeptide having
CC heparanase catalytic activity. The methods and compositions of the
CC present invention are useful for the prevention and/or treatment of
CC diseases or conditions associated with aberrant heparanase activity, such
CC as heparanase-dependent cancer, cancer, autoimmune reaction and
CC inflammation. The gene for human heparanase is located on chromosome 4.
CC The present sequence is a human heparanase cDNA.
XX

QQ Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match	99.9%	Score 1719.4	DB 12	Length 1721
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1720	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Qy 1	CTAGAGCTTTCGACTCTCCGCTGCGCGGACGCTGCGGGGGAGCAGCGAGTGAGCCCA	60		
Db 1	CTAGAGCTTTCGACTCTCCGCTGCGCGGACGCTGCGGGGGAGCAGCGAGTGAGCCCA	60		
Qy 61	AGATGCTGCTCGGCTCGAAGCTCGGCTGCGCGCGCGCTGATGCTGCTCTCTGGGGC	120		
Db 61	AGATGCTGCTCGGCTCGAAGCTCGGCTGCGCGCGCGCTGATGCTGCTCTCTGGGGC	120		
Qy 121	CGCTGGGTCCCTCTCCCTGCGCGCCCTGCGCCGCGCGCTGATGCTGCTCTCTGGGGC	180		
Db 121	CGCTGGGTCCCTCTCCCTGCGCGCCCTGCGCCGCGCGCTGATGCTGCTCTCTGGGGC	180		
Qy 181	ACCTGGACTTCTTCCACCCAGAGCGCGTGCAACCTGGTGAGCCCTCGTTCCTGTCGGTCA	240		
Db 181	ACCTGGACTTCTTCCACCCAGAGCGCGTGCAACCTGGTGAGCCCTCGTTCCTGTCGGTCA	240		
Qy 241	CCATTGAGCCCAACTGGCCACGACCGCGGGTTCCTATCCTCTCGGGTTCCTCAAGC	300		
Db 241	CCATTGAGCCCAACTGGCCACGACCGCGGGTTCCTATCCTCTCGGGTTCCTCAAGC	300		
Qy 301	TTCTGTACCTTGGCCAGAGGCTTGCTCTGCGGTACCTGAGGTTGGTGCCACCAAGACAG	360		
Db 301	TTCTGTACCTTGGCCAGAGGCTTGCTCTGCGGTACCTGAGGTTGGTGCCACCAAGACAG	360		
Qy 361	ACTTCCTAATTTTCGATCCCAAGAGGAATCAACCTTTGAGAGAGAAAGTTACTTGGCAAT	420		
Db 361	ACTTCCTAATTTTCGATCCCAAGAGGAATCAACCTTTGAGAGAGAAAGTTACTTGGCAAT	420		
Qy 421	CTCAAGTCAACAGGATATTTGCAAAATATGATGATCCATCCTCTGATGTGAGGAGAGT	480		
Db 421	CTCAAGTCAACAGGATATTTGCAAAATATGATGATCCATCCTCTGATGTGAGGAGAGT	480		
Qy 481	TACGGTGGAAATGSCCTACCAGAGGCAATTTGCTACTCCGAGAACACTACCAGAAAAGT	540		
Db 481	TACGGTGGAAATGSCCTACCAGAGGCAATTTGCTACTCCGAGAACACTACCAGAAAAGT	540		
Qy 541	TCAAGAAACAGCACCTTACTCAAGAAAGCTCTGTAGATGTGCTATACACTTTTTCGAACTGCT	600		
Db 541	TCAAGAAACAGCACCTTACTCAAGAAAGCTCTGTAGATGTGCTATACACTTTTTCGAACTGCT	600		

Db	541	TCAAGAAACAGCACCTTACTCAAGAAAGCTCTGTAGATGTGCTATACACTTTTTCGAAACTGCT	600
Qy	601	CAGGACTGGACTTGATCTTTGGGCTTAATCGCTTATTAAAGAACAGCAGATTTGCAGTGGGA	660
Db	601	CAGGACTGGACTTGATCTTTGGGCTTAATCGCTTATTAAAGAACAGCAGATTTGCAGTGGGA	660
Qy	661	ACAGTTCCTAATGTCTCAGTGTCTCTCGACTACTGCTCTTCCAAAGGGGTATAAACATTTCTT	720
Db	661	ACAGTTCCTAATGTCTCAGTGTCTCTCGACTACTGCTCTTCCAAAGGGGTATAAACATTTCTT	720
Qy	721	GGGAACTAGGCAATGAACCTTAAACAGTTTCTTAAAGAGGCTGATATTTTTCATCAATCGGT	780
Db	721	GGGAACTAGGCAATGAACCTTAAACAGTTTCTTAAAGAGGCTGATATTTTTCATCAATCGGT	780
Qy	781	CGCAGTTTAGGAGAAGATTTTATTCATTTGCATATAACTTCTAAGAAAGTCCACCTTCAAAA	840
Db	781	CGCAGTTTAGGAGAAGATTTTATTCATTTGCATATAACTTCTAAGAAAGTCCACCTTCAAAA	840
Qy	841	ATGCAAAACTCTATGGTCCCTGATGTTGCTCAGCTCGAAGAAAGACGGCTTAAGATGCTGA	900
Db	841	ATGCAAAACTCTATGGTCCCTGATGTTGCTCAGCTCGAAGAAAGACGGCTTAAGATGCTGA	900
Qy	901	AGAGCTTCTGAAAGGCTGGTGGAGAGTGAATGATTGATTCAGTTACATGGCATCACTACTATT	960
Db	901	AGAGCTTCTGAAAGGCTGGTGGAGAGTGAATGATTGATTCAGTTACATGGCATCACTACTATT	960
Qy	961	TGAATGCAACGGACTGCTTACCAGGGAGATTTTCTTAAACCTCTGATTTTGGACATTTTTTA	1020
Db	961	TGAATGCAACGGACTGCTTACCAGGGAGATTTTCTTAAACCTCTGATTTTGGACATTTTTTA	1020
Qy	1021	TTTTCATCTGTGCAAAAAGTTTTTCCAGGTGGTTCAGAGCACACAGGCTTGGCAAGAGTCT	1080
Db	1021	TTTTCATCTGTGCAAAAAGTTTTTCCAGGTGGTTCAGAGCACACAGGCTTGGCAAGAGTCT	1080
Qy	1081	GGTTAGGAGAAAACAAGCTCTGCATATGAGCGCGAGCGCCCTTGTCTATCCGACACCTTTG	1140
Db	1081	GGTTAGGAGAAAACAAGCTCTGCATATGAGCGCGAGCGCCCTTGTCTATCCGACACCTTTG	1140
Qy	1141	CAGCTGCGCTTATGTGGCTGGATATAATTTGGGCTGTGAGCCCGGATGGGAATAGAAAGTGG	1200
Db	1141	CAGCTGCGCTTATGTGGCTGGATATAATTTGGGCTGTGAGCCCGGATGGGAATAGAAAGTGG	1200
Qy	1201	TGATGAGGCAAGTATCTTTTGGAGCAGAGAACTACCAATTTAGTGGATGAAAACCTTCGATC	1260
Db	1201	TGATGAGGCAAGTATCTTTTGGAGCAGAGAACTACCAATTTAGTGGATGAAAACCTTCGATC	1260
Qy	1261	CTTTACCTGATTTATGGCTATCTCTTCTGTTCAAGAAATTTGGTGGGCACCAAGGTGTTAA	1320
Db	1261	CTTTACCTGATTTATGGCTATCTCTTCTGTTCAAGAAATTTGGTGGGCACCAAGGTGTTAA	1320
Qy	1321	TGGCAAGCGTCAAGGTTTCAAGAGAGAGAGCTTCGAGTATACCTTTCATTTGCAACAACA	1380
Db	1321	TGGCAAGCGTCAAGGTTTCAAGAGAGAGAGCTTCGAGTATACCTTTCATTTGCAACAACA	1380
Qy	1381	CTGACAACTCAAGGTATATAAGAGAGGAGATTTAACTCTGTATGCCATAAACTCCATTAACG	1440
Db	1381	CTGACAACTCAAGGTATATAAGAGAGGAGATTTAACTCTGTATGCCATAAACTCCATTAACG	1440
Qy	1441	TCACCAAGTACTTTCGGGTACCCTATCCTTTTCTAAACAAGCAAGTGGATGATTAACCTTC	1500
Db	1441	TCACCAAGTACTTTCGGGTACCCTATCCTTTTCTAAACAAGCAAGTGGATGATTAACCTTC	1500
Qy	1501	TAAGACCTTTGGGACCTCATGGATTTACTTTTCCAAATCTGTCCTCAACTCAATGGTCTAACTC	1560
Db	1501	TAAGACCTTTGGGACCTCATGGATTTACTTTTCCAAATCTGTCCTCAACTCAATGGTCTAACTC	1560
Qy	1561	TAAAGATGGTGGATGATCAAAACCTTGGCACTTAAATGGAAAAACCTCTCCGGCCAGGAA	1620
Db	1561	TAAAGATGGTGGATGATCAAAACCTTGGCACTTAAATGGAAAAACCTCTCCGGCCAGGAA	1620
Qy	1621	GTTTCACTGGGCTTGCACAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCCCAAGTTG	1680
Db	1621	GTTTCACTGGGCTTGCACAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCCCAAGTTG	1680

Qy 1681 CTGCTTGCATCTGAAATATAAATATACTAGTCTGACACTG 1721
 Db 1681 CTGCTTGCATCTGAAATATAAATATACTAGTCTGACACTG 1721

RESULT 10

ADM48717
 ID ADM48717 standard; cDNA; 1721 BP.

XX AC ADM48717;

XX 03-JUN-2004 (first entry)

XX Human hpa cDNA.

XX Transgenic animal; heparanase; cancer; viral infection; restenosis;
 KW neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa;
 XX human; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 63..1694

FT /*tag= a

FT /product= "Hpa protein"

XX US2003217375-A1.

XX 20-NOV-2003.

XX 24-FEB-2003; 2003US-00371218.

XX 31-AUG-1998; 98WO-US017954.

XX 01-MAR-1999; 99US-00258892.

XX 06-FEB-2001; 2001US-00776874.

XX 19-NOV-2001; 2001US-00988113.

XX (ZCHA/) ZCHARIA E.

XX (VLOD/) VLODAVSKY I.

XX (METZ/) METZGER S.

XX (PECK/) PECKER I.

XX (ILAN/) ILAN N.

XX (CHAJ/) CHAJEK-SHAUL T.

XX (GOLD/) GOLDSHMIDT O.

PI Zcharia E, Vlodavsky I, Metzger S, Pecker I, Ilan N;

PI Chajek-Shaul T, Goldshmidt O;

XX WPI; 2004-021918/02.

XX P-PSDB; ADM48716.

XX New transgenic non-human animal expressing heparinase, useful as models
 FT for human disease, such as cancers, viral infection, neurodegenerative
 FT diseases, restenosis, atherosclerosis and pulmonary disorders.

PS Example 1; SEQ ID NO 11; 106pp; English.

XX The present invention relates to a transgenic non-human animal whose
 CC genome comprises an exogenous polynucleotide sequence, including a
 CC promoter active in tissues of the non-human, a region encoding a human
 CC heparanase, where the promoter and the region encoding human heparanase
 CC are operably linked in the exogenous polynucleotide such that human
 CC heparanase is expressed in at least a portion of the cells of the non-
 CC human animal. The methods and compositions of the present invention are
 CC useful for the production of transgenic animals expressing heparanase, to
 CC be used as models for human diseases such as cancers, viral infection,
 CC restenosis, neurodegenerative diseases, atherosclerosis and pulmonary
 CC disorders. The present sequence is human hpa cDNA used in the
 CC exemplification of the invention.

XX Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match 99.9%; Score 1719.4; DB 12; Length 1721;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTAGAGCTTTGCACTCTCCGCTGCGGCGAGCTGCGGGGGAGACGACAGGTGAGGCCA 60
 Db 1 CTAGAGCTTTGCACTCTCCGCTGCGGCGAGCTGCGGGGGAGACGACAGGTGAGGCCA 60

Qy 61 AGATGCTGTGCTGCGCTCGAAGCCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 120
 Db 61 AGATGCTGTGCTGCGCTCGAAGCCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 120

Qy 121 CGCTGGGTCCCTCTCCCTGCGCGCTGCGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCG 180
 Db 121 CGCTGGGTCCCTCTCCCTGCGCGCTGCGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCG 180

Qy 181 ACCTGGACCTCTTCCACCCAGGAGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCG 240
 Db 181 ACCTGGACCTCTTCCACCCAGGAGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCG 240

Qy 241 CCATTGACGCCAACCTGGGCGACCGCGGTTCTCTCATCTCTCTCTCTCTCTCTCTCTCT 300
 Db 241 CCATTGACGCCAACCTGGGCGACCGCGGTTCTCTCATCTCTCTCTCTCTCTCTCTCTCT 300

Qy 301 TTCGTACCTTGGCCAGAGGCTTCTCTCTGCGTACCTGAGGTTTGGTGGCCACCAAGACAG 360
 Db 301 TTCGTACCTTGGCCAGAGGCTTCTCTCTGCGTACCTGAGGTTTGGTGGCCACCAAGACAG 360

Qy 361 ACTTCCTTAATTTTCGATCCCAAGAGGATCAACCTTTGAAGAGAGAGGTTACTGGCAAT 420
 Db 361 ACTTCCTTAATTTTCGATCCCAAGAGGATCAACCTTTGAAGAGAGAGGTTACTGGCAAT 420

Qy 421 CTCAGGTCAACAGGATATTTGCAAAATATGGATTCATCTCTCTCTCTCTCTCTCTCTCT 480
 Db 421 CTCAGGTCAACAGGATATTTGCAAAATATGGATTCATCTCTCTCTCTCTCTCTCTCTCT 480

Qy 481 TACGGTTGGAATGGCCCTACCAAGAGCAATGCTCTCTGAGAACACAGAGTTTGCAGTGA 540
 Db 481 TACGGTTGGAATGGCCCTACCAAGAGCAATGCTCTCTGAGAACACAGAGTTTGCAGTGA 540

Qy 541 TCAAGAACAGCAGCTACTCAAGAGCTCTGTAGATGTGTATACATCTTTTGCAGTGA 600
 Db 541 TCAAGAACAGCAGCTACTCAAGAGCTCTGTAGATGTGTATACATCTTTTGCAGTGA 600

Qy 601 CAGGACTGGACTTTGATCTTTGGCTAAATGCGTTATTAAGAACAGCAGATTTTGCAGTGA 660
 Db 601 CAGGACTGGACTTTGATCTTTGGCTAAATGCGTTATTAAGAACAGCAGATTTTGCAGTGA 660

Qy 661 ACAGTTCTAATGTCTCAGTTGCTCTGAGACTACTGCTCTTCCAAAGGGGTATAACATTTCTT 720
 Db 661 ACAGTTCTAATGTCTCAGTTGCTCTGAGACTACTGCTCTTCCAAAGGGGTATAACATTTCTT 720

Qy 721 GGAACCTAGCAATGACCTTAACAGTTTCTTAAAGGCTGATATTTTTCATCAATCGGT 780
 Db 721 GGAACCTAGCAATGACCTTAACAGTTTCTTAAAGGCTGATATTTTTCATCAATCGGT 780

Qy 781 CGCAGTTAGGAGAAAGATTTTATTTCAATTTGATATAAATTTCTTAAGAAAGTCCACCTTCAAAA 840
 Db 781 CGCAGTTAGGAGAAAGATTTTATTTCAATTTGATATAAATTTCTTAAGAAAGTCCACCTTCAAAA 840

Qy 841 ATCAAAATCTATGCTGCTGATGTTGGTTCAGCTCGAAGAACAGACGGCTTAAGTGTGA 900
 Db 841 ATCAAAATCTATGCTGCTGATGTTGGTTCAGCTCGAAGAACAGACGGCTTAAGTGTGA 900

Qy 901 AGAGCTTCTGAGGCTGGGAGAGTGAATTCAGTTACATTCAGTTCATCTACTACTATT 960
 Db 901 AGAGCTTCTGAGGCTGGGAGAGTGAATTCAGTTACATTCAGTTCATCTACTACTATT 960

Qy 961 TGAATGACGAGTCTGTACCAAGGAAAGATTTTCTAAACCTGTATGATTTGGACATTTT 1020
 Db 961 TGAATGACGAGTCTGTACCAAGGAAAGATTTTCTAAACCTGTATGATTTGGACATTTT 1020

Qy 1021 TTTTCATCTGTGCAAAAGATTTTCCAGGTGTTGAGAGCACAGGCTGGCAAGAGGTCT 1080

Db 1021 TTTTCATCTGTCAGAAAGATTTTCCAGGTGGTTGAGAGCACACGAGCCTGGCAAGGTCT 1080
Qy 1081 GGTAGAGAAAACAGCTCTGCATATAGAGCGGAGGCCCTTGTCTATTCGACACCTTTTG 1140
Db 1081 GGTAGAGAAAACAGCTCTGCATATAGAGCGGAGGCCCTTGTCTATTCGACACCTTTTG 1140
Qy 1141 CAGCTGGCTTTATGTGGCTGATAAATTTGGGCTGTGAGCCGATGGATAGAGTGG 1200
Db 1141 CAGCTGGCTTTATGTGGCTGATAAATTTGGGCTGTGAGCCGATGGATAGAGTGG 1200
Qy 1201 TGATGAGCAAGTATTTCTTTGGAGCAGGAAACTACCATTTAGTGGATGAAACTTCCGATC 1260
Db 1201 TGATGAGCAAGTATTTCTTTGGAGCAGGAAACTACCATTTAGTGGATGAAACTTCCGATC 1260
Qy 1261 CTTTACCTGATTTATGGCTATCTCTCTGTTCAAGAAATTTGGTGGCACCACCAAGGTGTA 1320
Db 1261 CTTTACCTGATTTATGGCTATCTCTCTGTTCAAGAAATTTGGTGGCACCACCAAGGTGTA 1320
Qy 1321 TGSCAAGCGTCAAGGTTCAAGAGAGGAGCTTCGAGTATACCTTCATTGCAACAACA 1380
Db 1321 TGGCAAGCGTCAAGGTTCAAGAGAGGAGCTTCGAGTATACCTTCATTGCAACAACA 1380
Qy 1381 CTGACAAATCCAAAGTATAAAGAGGAGATTTAACTCTGTATGCCATAAACCTCCATAACG 1440
Db 1381 CTGACAAATCCAAAGTATAAAGAGGAGATTTAACTCTGTATGCCATAAACCTCCATAACG 1440
Qy 1441 TCACAAGTACTTGGGTTACCTATCTCTTTTCTAAAGCAAGTGGATAAATACCTTC 1500
Db 1441 TCACAAGTACTTGGGTTACCTATCTCTTTTCTAAAGCAAGTGGATAAATACCTTC 1500
Qy 1501 TAAGACCTTTGGGACCTCATGATTAATTTCCAAATCTGTCCTCAACTCAATGGTCTAACTC 1560
Db 1501 TAAGACCTTTGGGACCTCATGATTAATTTCCAAATCTGTCCTCAACTCAATGGTCTAACTC 1560
Qy 1561 TAAAGATGGTGGATGATCAAAACCTTGCCACCTTTTAAATGGMAAAACCTCTCGGCGCAGAA 1620
Db 1561 TAAAGATGGTGGATGATCAAAACCTTGCCACCTTTTAAATGGMAAAACCTCTCGGCGCAGAA 1620
Qy 1621 GTTCACCTGGGCTTCCAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680
Db 1621 GTTCACCTGGGCTTCCAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680
Qy 1681 CTGCTTGCATCTGAATAAATAATATACTAGTCTTGACACTG 1721
Db 1681 CTGCTTGCATCTGAATAAATAATATACTAGTCTTGACACTG 1721

RESULT 11
ADM48715
ID ADM48715 standard; cDNA; 1721 BP.
XX AC
XX AC ADM48715;
XX AC
DT 03-JUN-2004 (first entry)
XX AC
DE Human hpa cDNA.
XX AC
KW Transgenic animal; heparanase; cancer; viral infection; restenosis;
KW neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa;
KW human; gene; ss.
XX AC
OS Homo sapiens.
XX AC
XX AC
FH Key Location/Qualifiers
FT CDS 63..1694
FT /*tag= a
FT /product= "Hpa protein"
XX AC
XX US2003217375-A1.
XX 20-NOV-2003.
XX AC

24-FEB-2003; 2003US-00371218.
31-AUG-1998; 98WO-US017954.
01-MAR-1999; 99US-00258892.
06-FEB-2001; 2001US-00776874.
19-NOV-2001; 2001US-00988113.
(ZCHA/) ZCHARIA E.
(VLJD/) VLJDAVSKY I.
(METZ/) METZGER S.
(PECK/) PECKER I.
(ILAN/) ILAN N.
(CHAJ/) CHAJEK-SHAUL T.
(GOLD/) GOLDSHMIDT O.
Zcharia E, Vlodayvsky I, Metzger S, Pecker I, Ilan N;
Chajek-Shaul T, Goldshmidt O;
WPI: 2004-021918/02.
P-PSDB; ADM48715.
New transgenic non-human animal expressing heparinase, useful as models
for human disease, such as cancers, viral infection, neurodegenerative
diseases, restenosis, atherosclerosis and pulmonary disorders.
Example 1; SEQ ID NO 9; 106pp; English.
The present invention relates to a transgenic non-human animal whose
genome comprises an exogenous polynucleotide sequence, including a
promoter active in tissues of the non-human, a region encoding a human
heparanase, where the promoter and the region encoding human heparanase
are operably linked in the exogenous polynucleotide such that human
heparanase is expressed in at least a portion of the cells of the non-
human animal. The methods and compositions of the present invention are,
useful for the production of transgenic animals expressing heparanase, to
be used as models for human diseases such as cancers, viral infection,
restenosis, neurodegenerative diseases, atherosclerosis and pulmonary
disorders. The present sequence is human hpa cDNA used in the
exemplification of the invention.
Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;
Query Match 99.9%; Score 1719, 4; DB 12; Length 1721;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CTAGAGCTTTTCGACTCTCCGCTGCGGGAGCTGGCGGGGGAGCAGCCAGGTGAGCCCA 60
Db 1 CTAGAGCTTTTCGACTCTCCGCTGCGGGAGCTGGCGGGGGAGCAGCCAGGTGAGCCCA 60
Qy 61 AGATGCTGCTGCGGCTCGAAGCCTTGCCTGCGCGCGCGCTGATGCTGCTGCTGCGGC 120
Db 61 AGATGCTGCTGCGGCTCGAAGCCTTGCCTGCGCGCGCGCTGATGCTGCTGCTGCGGC 120
Qy 121 CGCTGGGTCCCTCTCCCTGCGCGCCTGCGCGCGCGCTGATGCTGCTGCTGCGGC 180
Db 121 CGCTGGGTCCCTCTCCCTGCGCGCCTGCGCGCGCGCTGATGCTGCTGCTGCGGC 180
Qy 181 ACCTGGAATTTCTTACCCAGGAGCGCTGCACTGCTGAGCCCTCGTCTGCTGCTGCA 240
Db 181 ACCTGGAATTTCTTACCCAGGAGCGCTGCACTGCTGAGCCCTCGTCTGCTGCTGCA 240
Qy 241 CCATTGACGCAACCTGGCCACGAGCCCGGGTTCCTCATCTCTCTGGGTTCCTCAAGC 300
Db 241 CCATTGACGCAACCTGGCCACGAGCCCGGGTTCCTCATCTCTCTGGGTTCCTCAAGC 300
Qy 301 TTGCTACCTTTGGCCAGAGGCTTGTCTCTCGTACCTGAGGTTTGGTGGCACCAGACAG 360
Db 301 TTGCTACCTTTGGCCAGAGGCTTGTCTCTCGTACCTGAGGTTTGGTGGCACCAGACAG 360
Qy 361 ACTTCTTAATTTTCGATCCCAAGAGGAATCAACCTTTTGAAGAGAGAGTACTGGCAAT 420
Db 361 ACTTCTTAATTTTCGATCCCAAGAGGAATCAACCTTTTGAAGAGAGAGTACTGGCAAT 420

Qy	421	CTCAAGTCAACAGGATATTTGCAAAATATGGATCCATCCCTCCTGATGTGGAGGAGAAGT	480
Db	421	CTCAAGTCAACAGGATATTTGCAAAATATGGATCCATCCCTCCTGATGTGGAGGAGAAGT	480
Qy	481	TACGGTTGGAATGGCCCTACAGAGAGCAATGCTACTCCGAGAACACTACGAGAAAAGT	540
Db	481	TACGGTTGGAATGGCCCTACAGAGAGCAATGCTACTCCGAGAACACTACGAGAAAAGT	540
Qy	541	TCAAGAACAGCAGCCTACTCAAGAGCTCTGTAGATGTCTATACACTTTTGGCAAACTGCT	600
Db	541	TCAAGAACAGCAGCCTACTCAAGAGCTCTGTAGATGTCTATACACTTTTGGCAAACTGCT	600
Qy	601	CAGGACTGGACTTGATCTTTGGCCATAATGCGTTATTAAAGAACAGCAGATTTGCAGTGG	660
Db	601	CAGGACTGGACTTGATCTTTGGCCATAATGCGTTATTAAAGAACAGCAGATTTGCAGTGG	660
Qy	661	ACAGTTCTAATGCTCAGTTGCTCTGACACTACTGCTCTTCAAGGGGTATAAATTTCTT	720
Db	661	ACAGTTCTAATGCTCAGTTGCTCTGACACTACTGCTCTTCAAGGGGTATAAATTTCTT	720
Qy	721	GGGAACCTAGCAATGAACCTAAACAGTTTCTTAAGAGGCTGATATTTTTCATCAATGGGT	780
Db	721	GGGAACCTAGCAATGAACCTAAACAGTTTCTTAAGAGGCTGATATTTTTCATCAATGGGT	780
Qy	781	CGCAGTTAGGAGAGATTTTATTCAATTCATATAAATCTTAAAGAAAGTCCACCTTCAAAA	840
Db	781	CGCAGTTAGGAGAGATTTTATTCAATTCATATAAATCTTAAAGAAAGTCCACCTTCAAAA	840
Qy	841	ATGCAAACTCTATGCTGCTGATGTTGGTCAAGCTCGAAGAAAGAGCGCTAAGATGCTGA	900
Db	841	ATGCAAACTCTATGCTGCTGATGTTGGTCAAGCTCGAAGAAAGAGCGCTAAGATGCTGA	900
Qy	901	AGAGCTTCCTGAAGCTGTGGAGAGTGAATTCAGTTTCAATGCTATCATCTACTATT	960
Db	901	AGAGCTTCCTGAAGCTGTGGAGAGTGAATTCAGTTTCAATGCTATCATCTACTATT	960
Qy	961	TGAATGACCGGACTGCTACAGGGAAGATTTTCTAAACCTCTGATGTTTGGACATTTTAA	1020
Db	961	TGAATGACCGGACTGCTACAGGGAAGATTTTCTAAACCTCTGATGTTTGGACATTTTAA	1020
Qy	1021	TTTCACTGTGCAAAAAGTTTTCAGGTGTGAGAGCACAGCGCTGGCAAGAGTCT	1080
Db	1021	TTTCACTGTGCAAAAAGTTTTCAGGTGTGAGAGCACAGCGCTGGCAAGAGTCT	1080
Qy	1081	GGTTAGGAGAAACAAGCTCTGCATATGAGGCGGAGCGCCCTTCTATCCGACCTTTG	1140
Db	1081	GGTTAGGAGAAACAAGCTCTGCATATGAGGCGGAGCGCCCTTCTATCCGACCTTTG	1140
Qy	1141	CAGCTGGCTTTATGTGGCTGGATAAATTTGGGCTGTGAGCCCGAATGGGAATAGAAGTGG	1200
Db	1141	CAGCTGGCTTTATGTGGCTGGATAAATTTGGGCTGTGAGCCCGAATGGGAATAGAAGTGG	1200
Qy	1201	TGATGAGGCAAGTATCTTTGGAGCAGGAACTACCAATTTAGTGGATGAAAATCTCGATC	1260
Db	1201	TGATGAGGCAAGTATCTTTGGAGCAGGAACTACCAATTTAGTGGATGAAAATCTCGATC	1260
Qy	1261	CTTTACTGATTTATGCTATCTCTTCTGTTCAAGAAATTTGGTGGGACCAGAGTGTAA	1320
Db	1261	CTTTACTGATTTATGCTATCTCTTCTGTTCAAGAAATTTGGTGGGACCAGAGTGTAA	1320
Qy	1321	TGGCAAGCTGCAAGGTTTCAAGAGAGGAGGCTTCGAGTATACCTTCATTGCACAAACA	1380
Db	1321	TGGCAAGCTGCAAGGTTTCAAGAGAGGAGGCTTCGAGTATACCTTCATTGCACAAACA	1380
Qy	1381	CTGACATCAAGGTATAAAGAGGAGATTTAACTCTGTATGCCATAAACTCCATAACG	1440
Db	1381	CTGACATCAAGGTATAAAGAGGAGATTTAACTCTGTATGCCATAAACTCCATAACG	1440
Qy	1441	TCACCAAGTACTTGGCTTACCTATCTTTTCTTAACAGCAAGTGGATAATACCTTC	1500
Db	1441	TCACCAAGTACTTGGCTTACCTATCTTTTCTTAACAGCAAGTGGATAATACCTTC	1500
Qy	1501	TAAGACCTTTGGGACCTCATGGATTAATTTCCAAATCTGTCCAACTCAATGGTCTAACTC	1560
Db	1501	TAAGACCTTTGGGACCTCATGGATTAATTTCCAAATCTGTCCAACTCAATGGTCTAACTC	1560
Qy	1561	TAAAGATGTGGATGATCAAACTTGGCACCCTTTAATGGAAAAACCTCTCCGGCCAGGAA	1620
Db	1561	TAAAGATGTGGATGATCAAACTTGGCACCCTTTAATGGAAAAACCTCTCCGGCCAGGAA	1620
Qy	1621	GTTCACTGGGCTTGGCAGGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG	1680
Db	1621	GTTCACTGGGCTTGGCAGGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG	1680
Qy	1681	CTGCTTGCATCTGAAAATAAATAATATATAGTCTGACACTG 1721	
Db	1681	CTGCTTGCATCTGAAAATAAATAATATATAGTCTGACACTG 1721	
RESULT 12			
AEA42434			
ID	AEA42434 standard; cDNA; 1721 BP.		
XX	AC AEA42434;		
XX	AC AEA42434;		
DT	28-JUL-2005 (first entry)		
XX	Human heparanase encoding cDNA SEQ ID NO:12.		
DE	antibody; heparanase; antiinflammatory; vulnery; immunosuppressive;		
XX	antigenic; cytostatic; antiarteriosclerotic; vasotropic;		
KW	inflammation; wound healing; scarring; vasculopathy; autoimmune disease;		
KW	angiogenesis disorder; cancer; tumor; metastasis; gene; ss.		
XX	Homo sapiens.		
XX	Key		
XX	Location/Qualifiers		
FT	63..1694		
FT	/*tag= a		
FT	/product= "heparanase"		
FT	/transl_except= (pos:798..800,aa:Phe)		
FT	/note= "in SEQ ID NO:4, the corresponding protein in		
FT	figure 47 decodes exactly"		
XX	AU2004201462-A1.		
PN	06-MAY-2004.		
XX	08-APR-2004; 2004AU-00201462.		
XX	08-APR-2004; 2004AU-00201462.		
XX	(INSI-) INSIGHT BIOPHARMACEUTICALS LTD.		
PA	(HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.		
XX	Vlodavsky I, Pecker I, Miron M, Gilboa A, Miron D, Moskowitz H;		
PI	Shlomi Y, Peleg Y, Yacoby-Zeevi O, Ayal-Hershkovitz M, Ben-Artzi H;		
PI	Peinstein E;		
XX	WPI; 2005-173343/19.		
DR	P-PSDB; AEA42426, AEA42466.		
XX	Novel isolated antibody capable of specifically binding to epitope of		
PT	heparanase protein, useful for preventing and treating heparanase-related		
PT	disorder such as inflammatory disorder, scars, autoimmune conditions or		
PT	angiogenesis.		
XX	Example 7; SEQ ID NO 12; 260pp; English.		
PS	The invention relates to an isolated antibody or its portion (I) capable		
XX	of specifically binding to an epitope of a heparanase protein. Also		
CC	described: (1) a cell line (II) for producing a monoclonal antibody or		
CC	its portion, comprising a cell line for producing (I); (2) a		
CC	pharmaceutical composition comprising (I) and a carrier; and (3) an		
CC	affinity medium (III) for binding human heparanase polypeptides,		

CC comprising (I) immobilized to a chemically inert, insoluble carrier. (I)
CC useful for treating a subject suffering from a pathological condition,
CC which involves administering (I) to the subject. (I) is useful for
CC preventing and treating heparanase-related disorder or condition chosen
CC from inflammatory disorder, wound, scar, vasculopathy, autoimmune
CC condition, angiogenesis, cell proliferation, cancerous condition, tumor
CC cell proliferation, invasion of circulating tumor cells and metastatic
CC disease. (I) is useful for detecting the presence of heparanase
CC polypeptide in a sample. (I) is useful for detecting heparanase-related
CC disease or condition in a subject such as vertebrate, preferably mammal
CC e.g., human. The heparanase-related disorder or condition further
CC includes renal disease or disorder chosen from diabetic nephropathy,
CC glomerulosclerosis, nephrotic syndrome, minimal change nephrotic syndrome
CC and renal cell carcinoma. The present sequence encodes human heparanase,
CC which is used in the exemplification of the present invention.

XX
SQ Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match 99.9%; Score 1719.4; DB 14; Length 1721;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	CTAGAGCTTTGCACTCTCCGTCGCGCGCACTGCGCGGGGAGCAGCCAGGTGAGCCCA	60
Db	1	CTAGAGCTTTGCACTCTCCGTCGCGCGCACTGCGCGGGGAGCAGCCAGGTGAGCCCA	60
Qy	61	AGATGCTGCTGCGCTCGAAGCTGCTGCGCGCGCGCGCTGATGCTGCTGCTGGGC	120
Db	61	AGATGCTGCTGCGCTCGAAGCTGCTGCGCGCGCGCGCTGATGCTGCTGCTGGGC	120
Qy	121	CGCTGGGTGCCCTCTCCCTGCGCCCTGCCGCCGACCTGCGCAAGCAGGACGCTCGTG	180
Db	121	CGCTGGGTGCCCTCTCCCTGCGCCCTGCCGCCGACCTGCGCAAGCAGGACGCTCGTG	180
Qy	181	ACCTGGAATTTCTTCAACCCAGAGCGCTGCACTCTGCTGAGCCCTCGTCTGTCGCTCA	240
Db	181	ACCTGGAATTTCTTCAACCCAGAGCGCTGCACTCTGCTGAGCCCTCGTCTGTCGCTCA	240
Qy	241	CCATTGAGCGCAACTGGCCAGCAGCCGCGGTTCTCTATCCTCTGGTTCCTCAAGC	300
Db	241	CCATTGAGCGCAACTGGCCAGCAGCCGCGGTTCTCTATCCTCTGGTTCCTCAAGC	300
Qy	301	TTCTGTACTCTGGCCAGAGGCTTGCTCTCTGGTACCTGAGTTGGTGCCACCAAGACAG	360
Db	301	TTCTGTACTCTGGCCAGAGGCTTGCTCTCTGGTACCTGAGTTGGTGCCACCAAGACAG	360
Qy	361	ACTTCCTAAATTTTCGATCCCAAGAGGAACTCAACTTTGAGAGAGAGTTACTGGCAAT	420
Db	361	ACTTCCTAAATTTTCGATCCCAAGAGGAACTCAACTTTGAGAGAGAGTTACTGGCAAT	420
Qy	421	CTCAAGTCAACCGAGATTTTGCAAAATATGATCCATCCCTCTCTGATGTGGAGGAGAT	480
Db	421	CTCAAGTCAACCGAGATTTTGCAAAATATGATCCATCCCTCTCTGATGTGGAGGAGAT	480
Qy	481	TACCGTTGGATGCGCTTACAGAGCAATTTGCTACTCCGAGACACTACCAGAAAAGT	540
Db	481	TACCGTTGGATGCGCTTACAGAGCAATTTGCTACTCCGAGACACTACCAGAAAAGT	540
Qy	541	TCAAGAACAGCACCTACTCAAGAGCTCTGTAGATGTGCTATACACTTTTGCAAACTGCT	600
Db	541	TCAAGAACAGCACCTACTCAAGAGCTCTGTAGATGTGCTATACACTTTTGCAAACTGCT	600
Qy	601	CAGACTGGACTTGATCTTTGGCCCTAAATGGTTATTTAAGAACAGGATTTGCACTGGA	660
Db	601	CAGACTGGACTTGATCTTTGGCCCTAAATGGTTATTTAAGAACAGGATTTGCACTGGA	660
Qy	661	ACAGTTCTAATGCTCAGTTGCTCTGGACTACTGCTCTTCCAGGGGTATACATTTCTT	720
Db	661	ACAGTTCTAATGCTCAGTTGCTCTGGACTACTGCTCTTCCAGGGGTATACATTTCTT	720
Qy	721	GGGAACATAGGCAATGAACCTAACAGTTTCTTTAAGAGGCTGATATTTTCAATCAATGGGT	780
Db	721	GGGAACATAGGCAATGAACCTAACAGTTTCTTTAAGAGGCTGATATTTTCAATCAATGGGT	780

Qy	781	CGCAGTTAGGAGAGATTTTATTTCAATTCATATAAATCTTCTAAGAAAGTCCACCTTCAAAA	840
Db	781	CGCAGTTAGGAGAGATTTTATTTCAATTCATATAAATCTTCTAAGAAAGTCCACCTTCAAAA	840
Qy	841	ATGCAAAACTCTATGGTCTCTGATGTTGGTCTGAGCTCGAAGAAAGACGGCTTAAGATGCTGA	900
Db	841	ATGCAAAACTCTATGGTCTCTGATGTTGGTCTGAGCTCGAAGAAAGACGGCTTAAGATGCTGA	900
Qy	901	AGAGCTTCTGGAAGCTGGTGGAGAGATGATGATTCAGTTATCATGGCATCACTACTATT	960
Db	901	AGAGCTTCTGGAAGCTGGTGGAGAGATGATGATTCAGTTATCATGGCATCACTACTATT	960
Qy	961	TGAATGGAAGGACTGCTTACAGGAGAGATTTTCTTAAACCTGATGATTCGACATTTTAA	1020
Db	961	TGAATGGAAGGACTGCTTACAGGAGAGATTTTCTTAAACCTGATGATTCGACATTTTAA	1020
Qy	1021	TTTTCATCTGTGCAAAAAGTTTTTCCAGGTGGTTCGAGAGCACCAGGCTTGGCAAGAGTCT	1080
Db	1021	TTTTCATCTGTGCAAAAAGTTTTTCCAGGTGGTTCGAGAGCACCAGGCTTGGCAAGAGTCT	1080
Qy	1081	GGTTAGGAGAAAACAAGCTCTGATATGGAGCGGAGCGCCCTTGTCTATCCGACACCTTTG	1140
Db	1081	GGTTAGGAGAAAACAAGCTCTGATATGGAGCGGAGCGCCCTTGTCTATCCGACACCTTTG	1140
Qy	1141	CAGCTGCTTTATGTGCTGGATAAATTTGGGCTGTCTCAGCCCGAAATGGGAATAGAAGTGG	1200
Db	1141	CAGCTGCTTTATGTGCTGGATAAATTTGGGCTGTCTCAGCCCGAAATGGGAATAGAAGTGG	1200
Qy	1201	TGATGAGGCAAGTATTTCTTTGGAGCAGGAACTACCAATTTAGTGGATGAAAACCTTCGATC	1260
Db	1201	TGATGAGGCAAGTATTTCTTTGGAGCAGGAACTACCAATTTAGTGGATGAAAACCTTCGATC	1260
Qy	1261	CTTTACCTGATATGCGCTATCTCTCTTCAAGAAAATTTGGTGGGCAACCAAGGTGTTAA	1320
Db	1261	CTTTACCTGATATGCGCTATCTCTCTTCAAGAAAATTTGGTGGGCAACCAAGGTGTTAA	1320
Qy	1321	TGCAAGCGTGCAAGGTTCAAGAGAGGAAAGCTTCGAGTATACCTTTCATTGACACAACA	1380
Db	1321	TGCAAGCGTGCAAGGTTCAAGAGAGGAAAGCTTCGAGTATACCTTTCATTGACACAACA	1380
Qy	1381	CTGACAACTCAAGGTATATAAGAGAGGATTTAACTCTGTATGCCATAAACTCCATTAACG	1440
Db	1381	CTGACAACTCAAGGTATATAAGAGAGGATTTAACTCTGTATGCCATAAACTCCATTAACG	1440
Qy	1441	TCACCAAGTACTTGGGTTACCTATCCCTTTCCTAACAAGCAAGTGGATAAATACCTTC	1500
Db	1441	TCACCAAGTACTTGGGTTACCTATCCCTTTCCTAACAAGCAAGTGGATAAATACCTTC	1500
Qy	1501	TAAAGCCTTTGGGACCTCATGGATTTACTTTCCAAATCTGTCCAACTCAATGCTTAACCTC	1560
Db	1501	TAAAGCCTTTGGGACCTCATGGATTTACTTTCCAAATCTGTCCAACTCAATGCTTAACCTC	1560
Qy	1561	TAAAGATGGTGGATGATCAAAACCTTGGCACCTTTAATGGAAAAACCTCTCCGGCCAGGAA	1620
Db	1561	TAAAGATGGTGGATGATCAAAACCTTGGCACCTTTAATGGAAAAACCTCTCCGGCCAGGAA	1620
Qy	1621	GTTCACTGGGCTTCCAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG	1680
Db	1621	GTTCACTGGGCTTCCAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG	1680
Qy	1681	CTGCTTGCATCTGAAAATAAATAATATCTAGTCTCTGACACTG 1721	
Db	1681	CTGCTTGCATCTGAAAATAAATAATATCTAGTCTCTGACACTG 1721	

RESULT 13
AEA42435
ID AEA42435 standard; cdna; 1721 BP.
XX
XX AEA42435;
XX
DT 28-JUL-2005 (first entry)

XX DE Human heparanase encoding cDNA SEQ ID NO:13.
XX DE antibody; heparanase; antiinflammatory; vulnery; immunosuppressive;
KW antiangiogenic; cytostatic; antiarteriosclerotic; vasotropic;
KW inflammation; wound healing; scarring; vasculopathy; autoimmune disease;
KW angiogenesis disorder; cancer; tumor; metastasis; gene; ss.
OS Homo sapiens.
XX XX
XX Key Location/Qualifiers
FH 63..1694
FT CDS /*tag= a
FT /product= "heparanase"
FT /transl_except= (pos:798..800,aa:Phe)
FT /note= "in SEQ ID NO:4, the corresponding protein in
FT figure 47 decodes exactly"
XX XX
PN AU2004201462-A1.
XX XX
XX 06-MAY-2004.
XX XX
XX 08-APR-2004; 2004AU-00201462.
XX XX
XX 08-APR-2004; 2004AU-00201462.
XX XX
XX (INSI-) INSIGHT BIOPHARMACEUTICALS LTD.
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
XX XX
PI Vlodavsky I, Pecker I, Mimon M, Gilboa A, Miron D, Moskowitz H;
PI Shlomi Y, Peleg Y, Yacoby-Zeevi O, Ayal-Hershkovitz M, Ben-Artzi H;
PI Feinstein E;
XX XX
XX WPI: 2005-173343/19.
DR P-PSDB; AEA42426, AEA42466.
XX XX
XX Novel isolated antibody capable of specifically binding to epitope of
PT heparanase protein, useful for preventing and treating heparanase-related
PT disorder such as inflammatory disorder, scars, autoimmune conditions or
PT angiogenesis.
XX XX
PS Example 8; SEQ ID NO 13; 260pp; English.
XX XX
CC The invention relates to an isolated antibody or its portion (I) capable
CC of specifically binding to an epitope of a heparanase protein. Also
CC described: (1) a cell line (II) for producing a monoclonal antibody or
CC its portion, comprising a cell line for producing (I); (2) a
CC pharmaceutical composition comprising (I) and a carrier; and (3) an
CC affinity medium (III) for binding human heparanase polypeptides,
CC comprising (I) immobilized to a chemically inert, insoluble carrier. (I)
CC useful for treating a subject suffering from a pathological condition,
CC which involves administering (I) to the subject. (I) is useful for
CC preventing and treating heparanase-related disorder or condition chosen
CC from inflammatory disorder, wound, scar, vasculopathy, autoimmune
CC condition, angiogenesis, cell proliferation, cancerous condition, tumor
CC cell proliferation, invasion of circulating tumor cells and metastatic
CC disease. (I) is useful for detecting the presence of heparanase-
CC polypeptide in a sample. (I) is useful for detecting heparanase-related
CC disease or condition in a subject such as vertebrate, preferably mammal
CC e.g., human. The heparanase-related disorder or condition further
CC includes renal disease or disorder chosen from diabetic nephropathy,
CC glomerulosclerosis, nephrotic syndrome, minimal change nephrotic syndrome
CC and renal cell carcinoma. The present sequence encodes human heparanase,
CC which is used in the exemplification of the present invention.
XX XX
SQ Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;
Query Match 99.9%; Score 1719.4; DB 14; Length 1721;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 CTAGAGCTTTCGACTCTCCGCTCGCGGCGAGCTGGCGGGGAGCAGCCAGGTGAGGCCA 60
61 AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCGCGCTGATGCTGCTCTCTCGGGC 120
61 AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCGCGCTGATGCTGCTCTCTCGGGC 120
121 CGCTGGGTCCCTCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCC 180
121 CGCTGGGTCCCTCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCC 180
181 ACCTGGACTTCTTCCACCCAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
181 ACCTGGACTTCTTCCACCCAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
241 CCATTGAGCCAACTGGCCACGAGCCGCGGTTTCCTCATCTCTCTCTCTCTCTCTCTCTCTCA 300
241 CCATTGAGCCAACTGGCCACGAGCCGCGGTTTCCTCATCTCTCTCTCTCTCTCTCTCTCTCA 300
301 TTCGTACCTTGGCCAGAGGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
301 TTCGTACCTTGGCCAGAGGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
361 ACTTCTCTAATTTTCGATCCCAAGAGGAATCAACCTTTTGAAGAGAGAGTTCCTGCGCAAT 420
361 ACTTCTCTAATTTTCGATCCCAAGAGGAATCAACCTTTTGAAGAGAGAGTTCCTGCGCAAT 420
421 CTCAGTCAACACAGGATATTTGCAAAATATGATTCATCCCTCTCTCTCTCTCTCTCTCTCTCT 480
421 CTCAGTCAACACAGGATATTTGCAAAATATGATTCATCCCTCTCTCTCTCTCTCTCTCTCTCT 480
481 TAGCGTTGGAATGGCCCTTACACAGAGCAATGCTACTCCGAGAACACTACACAGAAAAGT 540
481 TAGCGTTGGAATGGCCCTTACACAGAGCAATGCTACTCCGAGAACACTACACAGAAAAGT 540
541 TCAAGAACAGCACTACTCAAGAGCTCTGTAGATGCTGTATACATTTTTCGAAAACCTGCT 600
541 TCAAGAACAGCACTACTCAAGAGCTCTGTAGATGCTGTATACATTTTTCGAAAACCTGCT 600
601 CAGGACTGGACTTGTATCTTTGGCTAAATGCGTTATTAAGAACAGCAGATTTTGCAGTGGGA 660
601 CAGGACTGGACTTGTATCTTTGGCTAAATGCGTTATTAAGAACAGCAGATTTTGCAGTGGGA 660
661 ACAGTCTTAATGCTAGTTGCTCTCTGAGCTACTGCTCTTCCAAAGGGGTATAAATTTCTT 720
661 ACAGTCTTAATGCTAGTTGCTCTCTGAGCTACTGCTCTTCCAAAGGGGTATAAATTTCTTCT 720
721 GGGAACTAGGCAATGAGTCTTAAAGAGGCTGATATTTTTCATCAATGGGT 780
721 GGGAACTAGGCAATGAGTCTTAAAGAGGCTGATATTTTTCATCAATGGGT 780
781 CGCAGTTAGGAGAAAGATTTTATTTCAATTGATATAAATTTCTAAGAAAGTCCACCTTTCAAAA 840
781 CGCAGTTAGGAGAAAGATTTATTTCAATTGATATAAATTTCTAAGAAAGTCCACCTTTCAAAA 840
841 ATGCAAAACTCTATGCTCTGATGTTGGTCTGAGCTCGAAGAAAGACGGCTAAGATGCTGA 900
841 ATGCAAAACTCTATGCTCTGATGTTGGTCTGAGCTCGAAGAAAGACGGCTAAGATGCTGA 900
901 AGAGCTTCTTGAAGGCTGGTGGAGAGTGAATGATTCAGTTACATGTCATCTACTATT 960
901 AGAGCTTCTTGAAGGCTGGTGGAGAGTGAATGATTCAGTTACATGTCATCTACTATT 960
961 TGAATGAGCGGACTGCTTACCCAGGAAAGATTTTCTAAACCTGTATGATTTGGAATTTT 1020
961 TGAATGAGCGGACTGCTTACCCAGGAAAGATTTTCTAAACCTGTATGATTTGGAATTTT 1020
1021 TTTTCATCTGTGCAAAAGATTTTCCAGTGGTGGAGAGCACCAGGCTTGGCAAGAGTCT 1080
1021 TTTTCATCTGTGCAAAAGATTTTCCAGTGGTGGAGAGCACCAGGCTTGGCAAGAGTCT 1080
1081 GGTTAGGAGAAACAGCTCTGCATATGAGGCGGAGGCGCTTGTCTATCCGACACCTTTG 1140
1081 GGTTAGGAGAAACAGCTCTGCATATGAGGCGGAGGCGCTTGTCTATCCGACACCTTTG 1140

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Qy 1141 CAGCTGGCTTTATGTGGCTGATAAATTGGGCCCTGTGAGCCCGAATGGGAATAGAGTGG 1200
Db 1141 CAGCTGGCTTTATGTGGCTGATAAATTGGGCCCTGTGAGCCCGAATGGGAATAGAGTGG 1200
Qy 1201 TGATGAGCAAGTATTCTTTGGAGCAGGAAACTACCAATTTAGTGGATGAAACTTCGATC 1260
Db 1201 TGATGAGCAAGTATTCTTTGGAGCAGGAAACTACCAATTTAGTGGATGAAACTTCGATC 1260
Qy 1261 CTTTACCTGATATTGGCTATCTCTCTGTTCAAGAAATTTGGTGGGCACCAAGGTGTAA 1320
Db 1261 CTTTACCTGATATTGGCTATCTCTCTGTTCAAGAAATTTGGTGGGCACCAAGGTGTAA 1320
Qy 1321 TGSCAAGCGTCAAGGTTCAAGAGAGGAGCTTCGAGTATACCTTCATTTGCACAACA 1380
Db 1321 TGGCAAGCGTCAAGGTTCAAGAGAGGAGCTTCGAGTATACCTTCATTTGCACAACA 1380
Qy 1381 CTGCAATCCAAAGGTATAAGAGGAGATTTAACTCTGTATGCCATAAACCTCCATAACG 1440
Db 1381 CTGCAATCCAAAGGTATAAGAGGAGATTTAACTCTGTATGCCATAAACCTCCATAACG 1440
Qy 1441 TCACCAAGTACTTGGGTTACCTTATCTTTTCTAACAGCAAGTGGATAAATACCTTC 1500
Db 1441 TCACCAAGTACTTGGGTTACCTTATCTTTTCTAACAGCAAGTGGATAAATACCTTC 1500
Qy 1501 TAAGACCTTTGGGACCTCATGATTTACTTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560
Db 1501 TAAGACCTTTGGGACCTCATGATTTACTTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560
Qy 1561 TAAAGATGGTGGATGATCAAACTTGGCACCTTTAAATGGAAAAACCTCTCGGCGCAGGAA 1620
Db 1561 TAAAGATGGTGGATGATCAAACTTGGCACCTTTAAATGGAAAAACCTCTCGGCGCAGGAA 1620
Qy 1621 GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGTGATAGAAAATGCCAAAGTTG 1680
Db 1621 GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGTGATAGAAAATGCCAAAGTTG 1680
Qy 1681 CTGCTTGCATCTGAAATATAATATACTAGTCTTGACACTG 1721
Db 1681 CTGCTTGCATCTGAAATATAATATACTAGTCTTGACACTG 1721
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RESULT 14

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AA335650
ID AA335650 standard; cdna; 1899 BP.
AC AA335650;
XX
DT 09-JUL-1999 (first entry)
DE
DE cDNA encoding a human heparanase protein.
XX
KW Heparanase; hpa; modulator; heparin-binding growth factor;
KW cellular response; cytokine; cell interaction; plasma lipoprotein;
KW cellular susceptibility; infection; disintegration;
KW neurodegenerative plaque; wound healing; angiogenesis; restenosis;
KW atherosclerosis; inflammation; neurodegenerative disease; neurallise;
KW plasma heparin; micrometastasis; autoimmune lesion; renal failure; ss.
XX
OS Homo sapiens.
XX
XX WO9911798-A1.
XX
PD 11-MAR-1999.
XX
XX 31-AUG-1998; 98WO-US017954.
XX
PR 02-SEP-1997; 97US-00922170.
PR 02-JUL-1998; 98US-00109386.
XX
XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX (FRIE/) FRIEDMAN M M.
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XX
PI Pecker I, Vlodavsky I, Feinstein E;
XX
DR WPI; 1999-302255/25.
XX P-PSDB; AAY02346.
XX
PT New human polynucleotide useful for treating angiogenesis, restenosis,
XX and inflammation.
XX
PS Claim 4; Page 64-65; 63pp; English.
XX
XX The specification describes a polypeptide having heparanase (hpa)
CC activity. The recombinant protein is used as a modulator of heparin-
CC binding growth factors, cellular responses to heparin-binding growth
CC factors and cytokines, cell interaction with plasma lipoproteins,
CC cellular susceptibility to viral, protozoal and bacterial infections or
CC disintegration of neurodegenerative plaques. Heparanase may be useful for
CC conditions such as wound healing, angiogenesis, restenosis,
CC atherosclerosis, inflammation, neurodegenerative diseases, and viral
CC infections. Mammalian heparanase can be used to neutralize plasma
CC heparin, and anti-heparanase antibodies may be applied for
CC immunodetection and diagnosis of micrometastases, autoimmune lesions, and
CC renal failure in biopsy specimens, plasma samples, and body fluids. The
CC present sequence encodes human heparanase
XX
SQ Sequence 1899 BP; 495 A; 433 C; 510 G; 461 T; 0 U; 0 Other;
XX
Query Match 99.8%; Score 1717.8; DB 2; Length 1899;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1719; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CTAGAGCTTTCGACTCTCCGCTGCGGGCAGCTGGCGGGGAGCAGCAGGTGAGCCCA 60
Db 179 CTAGAGCTCTGACTCTCCGCTGCGGGCAGCTGGCGGGGAGCAGCAGGTGAGCCCA 238
Qy 61 AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCGCTGATGCTGCTCTCTGGGGC 120
Db 239 AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCGCTGATGCTGCTCTCTGGGGC 298
Qy 121 CGCTGGGTCCCTCTCTCCCTGGGGCCCTGCGCGCGCGCTGCGCGCGCGCTGCTGCTGG 180
Db 299 CGCTGGGTCCCTCTCTCCCTGGGGCCCTGCGCGCGCGCTGCGCGCGCGCTGCTGCTGG 358
Qy 181 ACCTGAGCTTCTTCAACCCAGGAGCGCTGACCTGGTGAGCCCTCTCTCTCTCTCTCA 240
Db 359 ACCTGAGCTTCTTCAACCCAGGAGCGCTGACCTGGTGAGCCCTCTCTCTCTCTCTCA 418
Qy 241 CCATTGACGCAACCTTGGCCACGAGCCCGCGGTTCTCTATCTCTCTCTCTCTCTCA 300
Db 419 CCATTGACGCAACCTTGGCCACGAGCCCGCGGTTCTCTATCTCTCTCTCTCTCTCA 478
Qy 301 TTCGTACTTGGCCAGAGGCTTGTCTCTCGTACTGAGCTTGTGGGACCGACAGACAG 360
Db 479 TTCGTACTTGGCCAGAGGCTTGTCTCTCGTACTGAGCTTGTGGGACCGACAGACAG 538
Qy 361 ACTTCTTAATTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGAGTACTTGGCAAT 420
Db 539 ACTTCTTAATTTTCGATCCCAAGAGGAATCAACCTTTGAAGAGAGAGTACTTGGCAAT 598
Qy 421 CTCAAGTCAACCCAGGATATTTGCAAAATATGGATCCATCTCTCTCTCTCTCTCTCT 480
Db 599 CTCAAGTCAACCCAGGATATTTGCAAAATATGGATCCATCTCTCTCTCTCTCTCTCT 658
Qy 481 TAGCGTTGGAATGGCCCTTACAGAGCAATTTGCTACTCCGAGAACTACACAGAAAAAGT 540
Db 659 TAGCGTTGGAATGGCCCTTACAGAGCAATTTGCTACTCCGAGAACTACACAGAAAAAGT 718
Qy 541 TCAAGAACAGCAGCTACTCTCAAGAGCTCTGTAGATGTCTATACACTTTTGCACAACTGCT 600
Db 719 TCAAGAACAGCAGCTACTCTCAAGAGCTCTGTAGATGTCTATACACTTTTGCACAACTGCT 778
Qy 601 CAGGACTGGACTTGTATCTTTGGCCCTAAATCGTTTATTGAAGAACAGAGATTGTCAGTGG 660
XX
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Db 779 CAGACTGGACTTGATCTTTGGCCCTAAATGCGTTATTAAAGAACAGCAGATTTGCGTGG 838
Qy 661 ACAGTTCTTAATGCTCAGTTGCTCTCGGACTACTGCTCTTCCAGAGCGGTATAACATTTCTT 720
Db 839 ACAGTTCTTAATGCTCAGTTGCTCTCGGACTACTGCTCTTCCAGAGCGGTATAACATTTCTT 898
Qy 721 GGGAACTAGGCAATGAACCTAACAGTTTCCTTAAGAGCGGTGATATTTTCATCAATGGGT 780
Db 899 GGGAACTAGGCAATGAACCTAACAGTTTCCTTAAGAGCGGTGATATTTTCATCAATGGGT 958
Qy 781 CGCAGTTAGGAGAGAGATTTTATCAATGTCATTAACCTTCTAAGAAAGCTCCACCTTCAAAA 840
Db 959 CGCAGTTAGGAGAGAGATTTTATCAATGTCATTAACCTTCTAAGAAAGCTCCACCTTCAAAA 1018
Qy 841 ATGCAAACTCTATGTCCTGATCTTGGTCAGCCCTCGAAGAAAGCGCTAAGATGCTGA 900
Db 1019 ATGCAAACTCTATGTCCTGATCTTGGTCAGCCCTCGAAGAAAGCGCTAAGATGCTGA 1078
Qy 901 AGAGCTTCCTGAAGGCTGGTGAGAGAGTATGATTCAGTTACATGCGATCACTACTATT 960
Db 1079 AGAGCTTCCTGAAGGCTGGTGAGAGAGTATGATTCAGTTACATGCGATCACTACTATT 1138
Qy 961 TGAATGACCGGACTGCTACGAGGAAGATTTTCTAACCCTGATGATTTGGACATTTTAA 1020
Db 1139 TGAATGACCGGACTGCTACGAGGAAGATTTTCTAACCCTGATGATTTGGACATTTTAA 1198
Qy 1021 TTTTCATCTGTCAAAAAGTTTTCAGGCTGGTTGAGAGCACCGAGCCCTGGCAAGAGTCT 1080
Db 1199 TTTTCATCTGTCAAAAAGTTTTCAGGCTGGTTGAGAGCACCGAGCCCTGGCAAGAGTCT 1258
Qy 1081 GGTTCAGAGAAACAAAGCTCTGCATATGAGAGCGGAGCGCCCTTGCTATCCGACACCTTTG 1140
Db 1259 GGTTCAGAGAAACAAAGCTCTGCATATGAGAGCGGAGCGCCCTTGCTATCCGACACCTTTG 1318
Qy 1141 CAGCTGCTTTATGCTGCTGATTAATTTGGCCCTGTGAGCCGAGTGGATAGAGTGG 1200
Db 1319 CAGCTGCTTTATGCTGCTGATTAATTTGGCCCTGTGAGCCGAGTGGATAGAGTGG 1378
Qy 1201 TGATGAGCGAAGTATCTTTGGAGCAGGAACCTACCTATGATGGAATGAACCTTCGATC 1260
Db 1379 TGATGAGCGAAGTATCTTTGGAGCAGGAACCTACCTATGATGGAATGAACCTTCGATC 1438
Qy 1261 CTTTACCTGATTAATGCTATCTCTTCTGTTCAAGAAATTTGGTGGGCGACCAAGGTGTTAA 1320
Db 1439 CTTTACCTGATTAATGCTATCTCTTCTGTTCAAGAAATTTGGTGGGCGACCAAGGTGTTAA 1498
Qy 1321 TGGCAAGCGTCAGGTTCAAGAGAGGAGCTTCGAGTATACCTTCATGTCACAAACA 1380
Db 1499 TGGCAAGCGTCAGGTTCAAGAGAGGAGCTTCGAGTATACCTTCATGTCACAAACA 1558
Qy 1381 CTGACAATCCAAGGTATAAGAGAGGAGATTTAACTCTGTATGTCATAAACCTCCATAACG 1440
Db 1559 CTGACAATCCAAGGTATAAGAGAGGAGATTTAACTCTGTATGTCATAAACCTCCATAACG 1618
Qy 1441 TCACCAAGTACTTCGGGTACCTCTATCTTTTCTAACAAGCAAGTGGATAAATACCTTC 1500
Db 1619 TCACCAAGTACTTCGGGTACCTCTATCTTTTCTAACAAGCAAGTGGATAAATACCTTC 1678
Qy 1501 TAAGACCTTTGGGACCTCATGATTAATCTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560
Db 1679 TAAGACCTTTGGGACCTCATGATTAATCTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1738
Qy 1561 TAAAGATGGTGATGATCAACCTTGGCCACTTTAATGGAACCACTCTCGGCGCAGAA 1620
Db 1739 TAAAGATGGTGATGATCAACCTTGGCCACTTTAATGGAACCACTCTCGGCGCAGAA 1798
Qy 1621 GTTCACCTGGGCTGCCAGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680
Db 1799 GTTCACCTGGGCTGCCAGCTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1858
Qy 1681 CTGCTTGCATCTGAAAAATAAATAATATCTAGTCTCGACACTG 1721
Db 1859 CTGCTTGCATCTGAAAAATAAATAATATCTAGTCTCGACACTG 1899
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RESULT 15

AAA75053

ID AAA75053 standard; cDNA; 1899 BP.

XX

AC AAA75053;

XX

DT 15-JAN-2001 (first entry)

XX

XX cDNA encoding a human heparanase polypeptide.

DE

XX

KW Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;

KW heparin-binding growth factor; cytokine; neurodegenerative plaque;

KW wound healing; infection; burn; angiogenesis; restenosis;

KW atherosclerosis; inflammation; neurodegenerative disease;

KW Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; ds.

XX

OS Homo sapiens.

XX

XX

FH Key Location/Qualifiers

FT CDS

FT 94..1872

FT /*tag= a

FT /product= "heparanase"

XX

PN WO200052178-A1.

XX

XX

PD 08-SEP-2000.

XX

PF 14-FEB-2000; 2000WO-US003542.

XX

XX

PR 01-MAR-1999; 99US-00258892.

XX

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PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.

PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

PA (FRIE/) FRIEDMAN M M.

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PI Pecker I, Vlodavsky I, Feinstein E;

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WPI; 2000-579289/54.

DR

P-PSDB; AAB08850.

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SQ Sequence 1899 BP; 495 A; 433 C; 510 G; 461 T; 0 U; 0 Other;

Query Match

Best Local Similarity 99.8%; Score 1717.8; DB 3; Length 1899;

Matches 1719; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTAGAGCTTCGACTCTCCGCTGGCGGAGCTGGCGGGGAGCAGCCAGGTGAGCCCA 60

Db 179 CTAGAGCTTCGACTCTCCGCTGGCGGAGCTGGCGGGGAGCAGCCAGGTGAGCCCA 238

Qy 61 AGATGCTGCTGCGCTCGAAGCTGCGCTGCCGCGCGCTGATGCTGCTGCTGCTGCGGC 120
Db |||||
Qy 239 AGATGCTGCTGCGCTCGAAGCTGCGCTGCCGCGCGCTGATGCTGCTGCTGCTGCGGC 298
Db |||||
Qy 121 CGCTGGGTCCCTCTCCCTCGCGCCCTGCCCCGACCTGCGCAAGCAAGCAAGCAAGCTCGTG 180
Db |||||
Qy 299 CGCTGGGTCCCTCTCCCTCGCGCCCTGCCCCGACCTGCGCAAGCAAGCAAGCAAGCTCGTG 358
Db |||||
Qy 181 ACCTGGGACTCTTCAACAGAGCGCTGCAAGCTGCTGAGCGCCCTGCTGCTGCTGCTGCA 240
Db |||||
Qy 359 ACCTGGGACTCTTCAACAGAGCGCTGCAAGCTGCTGAGCGCCCTGCTGCTGCTGCTGCA 418
Db |||||
Qy 241 CCATTGAGCGCAACCTGCGCCAGGACCGCGCGCTTCTCATCTCTGCTGCTGCTGCTGCAAGC 300
Db |||||
Qy 419 CCATTGAGCGCAACCTGCGCCAGGACCGCGCGCTTCTCATCTCTGCTGCTGCTGCTGCAAGC 478
Db |||||
Qy 301 TTGCTGACTTGGCGAGAGGCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCAAGC 360
Db |||||
Qy 479 TTGCTGACTTGGCGAGAGGCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCAAGC 538
Db |||||
Qy 361 ACTTCCCTAAATTTTCGATCCCAAGAGGAACTCAACCTTTGAGAGAGAGGTTACTTGGCAAT 420
Db |||||
Qy 539 ACTTCCCTAAATTTTCGATCCCAAGAGGAACTCAACCTTTGAGAGAGAGGTTACTTGGCAAT 598
Db |||||
Qy 421 CTCAAGTCAACAGAGATATTTGCAAAATATGATCCATCCCTCTGATGCTGAGAGAGAGT 480
Db |||||
Qy 599 CTCAAGTCAACAGAGATATTTGCAAAATATGATCCATCCCTCTGATGCTGAGAGAGAGT 658
Db |||||
Qy 481 TACGTTTGGAAATGCCCTTACAGGAGCAATTTGCTACTCCGAGAACACTTACACAGAAAAAGT 540
Db |||||
Qy 659 TACGTTTGGAAATGCCCTTACAGGAGCAATTTGCTACTCCGAGAACACTTACACAGAAAAAGT 718
Db |||||
Qy 541 TCAAGACAGACACTTACTCAAGAGCTCTGATGATGCTGATGCTGATGCTGATGCTGATGCTGAT 600
Db |||||
Qy 719 TCAAGACAGACACTTACTCAAGAGCTCTGATGATGCTGATGCTGATGCTGATGCTGATGCTGAT 778
Db |||||
Qy 601 CAGGACTGGACTTGATCTTTGGCTTAAATGGTTTAAAGAACAGCAGATTTGAGTGGGA 660
Db |||||
Qy 779 CAGGACTGGACTTGATCTTTGGCTTAAATGGTTTAAAGAACAGCAGATTTGAGTGGGA 838
Db |||||
Qy 661 ACAGTTCTAATGCTCAGTTGCTCTGGAATCTGCTCTTCCAGGGGTATACATTTCTT 720
Db |||||
Qy 839 ACAGTTCTAATGCTCAGTTGCTCTGGAATCTGCTCTTCCAGGGGTATACATTTCTT 898
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Qy 781 CGCAGTTAGGAGAGATTTTATTCAATTTGCAATAAATTTCTAAGAAAGTCCACCTTCAAAA 840
Db |||||
Qy 959 CGCAGTTAGGAGAGATTTTATTCAATTTGCAATAAATTTCTAAGAAAGTCCACCTTCAAAA 1018
Db |||||
Qy 841 ATGCAAAATCTATGCTGCTGATGTTGGTCAAGCTCGAAGAAAGACGCTTAAGATGCTGA 900
Db |||||
Qy 1019 ATGCAAAATCTATGCTGCTGATGTTGGTCAAGCTCGAAGAAAGACGCTTAAGATGCTGA 1078
Db |||||
Qy 901 AGAGCTTCTGAAGGCTGGTGGAGAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 960
Db |||||
Qy 1079 AGAGCTTCTGAAGGCTGGTGGAGAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 1138
Db |||||
Qy 961 TGAATGAGAGGACTGCTACAGGGAAGATTTTCTAAGACCTGATGATGATGATGATGATGATGAT 1020
Db |||||
Qy 1139 TGAATGAGAGGACTGCTACAGGGAAGATTTTCTAAGACCTGATGATGATGATGATGATGATGAT 1198
Db |||||
Qy 1021 TTTCATCTGTGCAAAAAAGTTTTTCCAGGTGGTTGAGAGCACCAAGGCTGGCAAGAGGTCT 1080
Db |||||
Qy 1199 TTTCATCTGTGCAAAAAAGTTTTTCCAGGTGGTTGAGAGCACCAAGGCTGGCAAGAGGTCT 1258
Db |||||
Qy 1081 GGTTAGGAGAAACAGCTCTGCATATAGGAGCGGAGCGCCCTTCTGATCCGACACCTTTG 1140
Db |||||
Qy 1259 GGTTAGGAGAAACAGCTCTGCATATAGGAGCGGAGCGCCCTTCTGATCCGACACCTTTG 1318
Db |||||
Qy 1141 CAGCTGGCTTTATGTGGCTGGATAAAATTTGGGCTGTGTCAGCCCGAATGGGAATAGAAGTGG 1200

Db |||||
Qy 1319 CAGCTGGCTTTATGTGCTGATATAATTTGGGCTGTGAGCCCGAATAGGAAGTGG 1378
Db |||||
Qy 1201 TGATGAGCAAGTATTTCTTTGGAGCAGGAAACTACCAATTTAGTGGATGAAATTTGCAATC 1260
Db |||||
Qy 1379 TGATGAGCAAGTATTTCTTTGGAGCAGGAAACTACCAATTTAGTGGATGAAATTTGCAATC 1438
Db |||||
Qy 1261 CTTTACCTGATTAATGGCTATCTCTCTGTTCAAGAAATTTGGTGGGACCAAGGTGTAA 1320
Db |||||
Qy 1439 CTTTACCTGATTAATGGCTATCTCTCTGTTCAAGAAATTTGGTGGGACCAAGGTGTAA 1498
Db |||||
Qy 1321 TGGCAAGCGTGCAGAGTTTCAAGAGAGGAGGATTTAACTCTGTATGCCATAAACTCCATTAACG 1380
Db |||||
Qy 1499 TGGCAAGCGTGCAGAGTTTCAAGAGAGGAGGATTTAACTCTGTATGCCATAAACTCCATTAACG 1558
Db |||||
Qy 1381 CTGACAAATCCAAGGTATAAAGAGAGGAGATTTAACTCTGTATGCCATAAACTCCATTAACG 1440
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Qy 1559 CTGACAAATCCAAGGTATAAAGAGAGGAGATTTAACTCTGTATGCCATAAACTCCATTAACG 1618
Db |||||
Qy 1441 TCACCAAGTACTTGGCGTTACCTATCCTTTTCTAACAAGCAAGTGGATAAACTCCATTAACG 1500
Db |||||
Qy 1619 TCACCAAGTACTTGGCGTTACCTATCCTTTTCTAACAAGCAAGTGGATAAACTCCATTAACG 1678
Db |||||
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Db |||||
Qy 1679 TAAAGACCTTTGGGACCTCATGGATTTACTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1738
Db |||||
Qy 1561 TAAAGATGGTGGATGATCAAACTTTGCCACCTTTTAAATGGAAAAAACCCTCTCCGGCCAGGAA 1620
Db |||||
Qy 1739 TAAAGATGGTGGATGATCAAACTTTGCCACCTTTTAAATGGAAAAAACCCTCTCCGGCCAGGAA 1798
Db |||||
Qy 1621 GTTCACTGGGCTTCCAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680
Db |||||
Qy 1799 GTTCACTGGGCTTCCAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1858
Db |||||
Qy 1681 CTGCTTGCATCTGAAAAATAAATAATATCTAGTCTGACACTG 1721
Db |||||
Qy 1859 CTGCTTGCATCTGAAAAATAAATAATATCTAGTCTGACACTG 1899

Search completed: February 28, 2006, 05:05:55

Job time : 1074 secs